

FIG. 1A

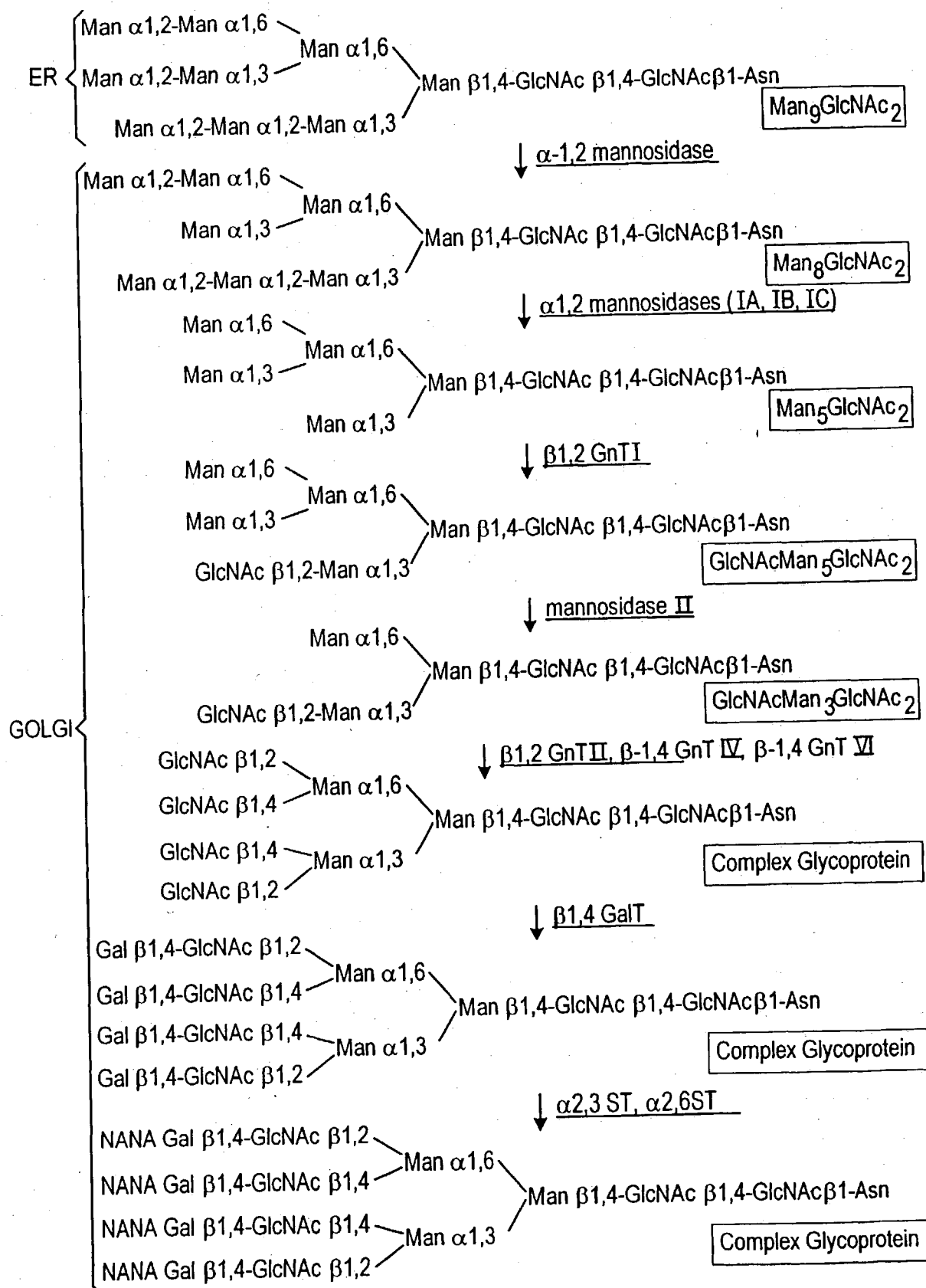


FIG. 1B

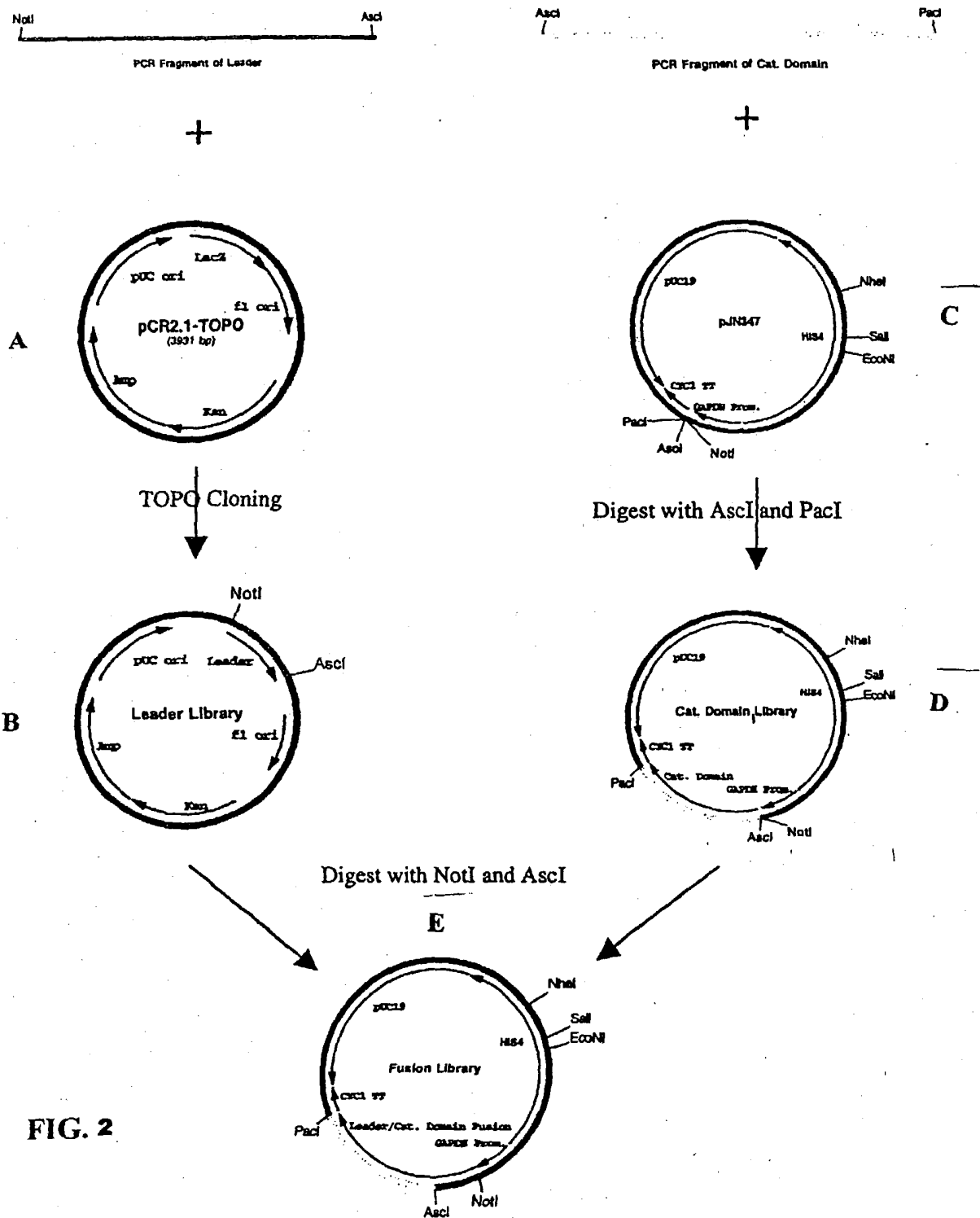


FIG. 2

FIG. 3

M. musculus alpha-1,2-mannosidase IA open reading frame. The transmembrane and catalytic domains are highlighted in bold respectively. The sequence of the primers used to generate the N-terminal truncations are highlighted by underlining and the start of each respective protein fragment indicated by an arrow.

[illegible]

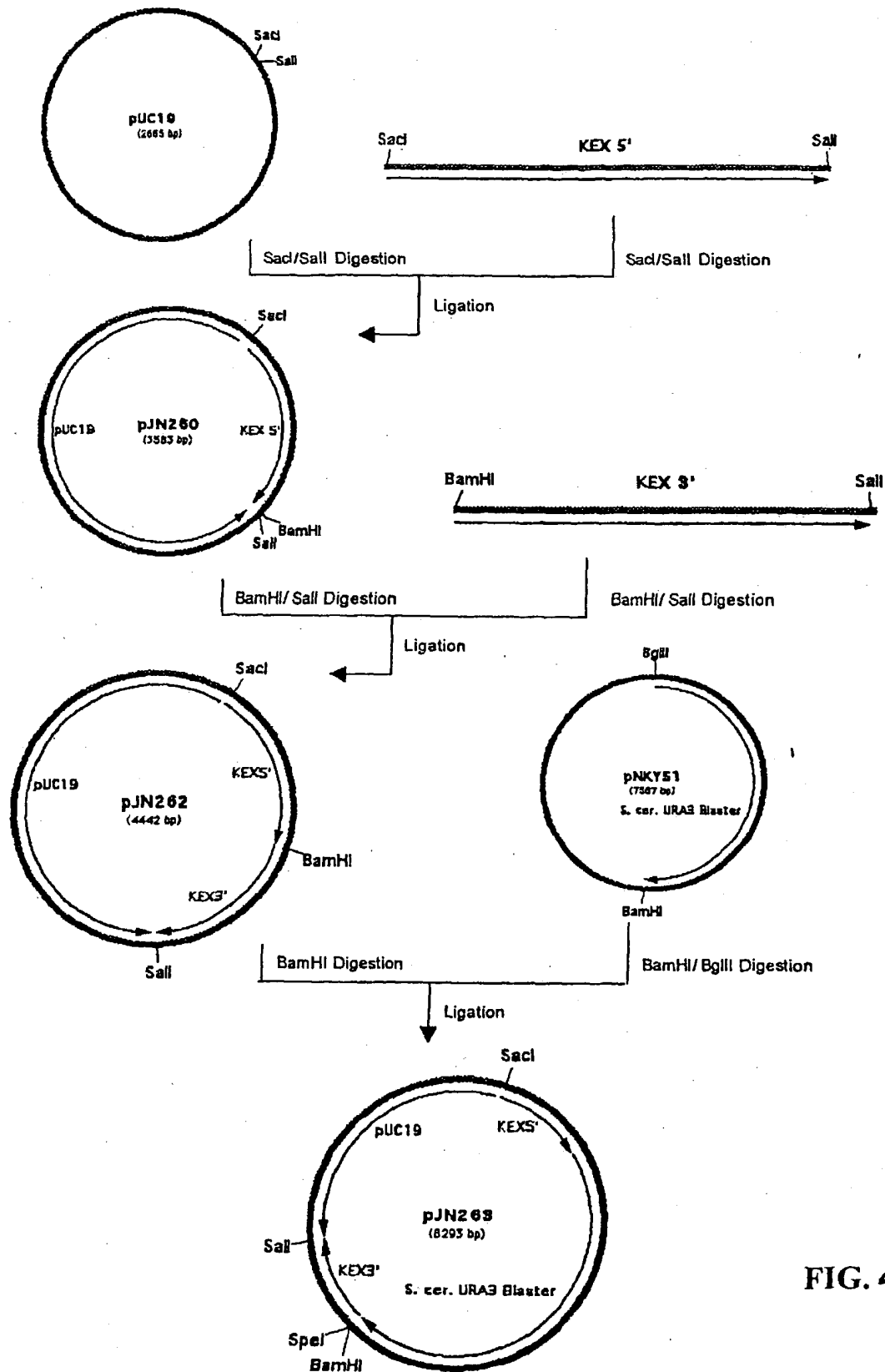


FIG. 4A

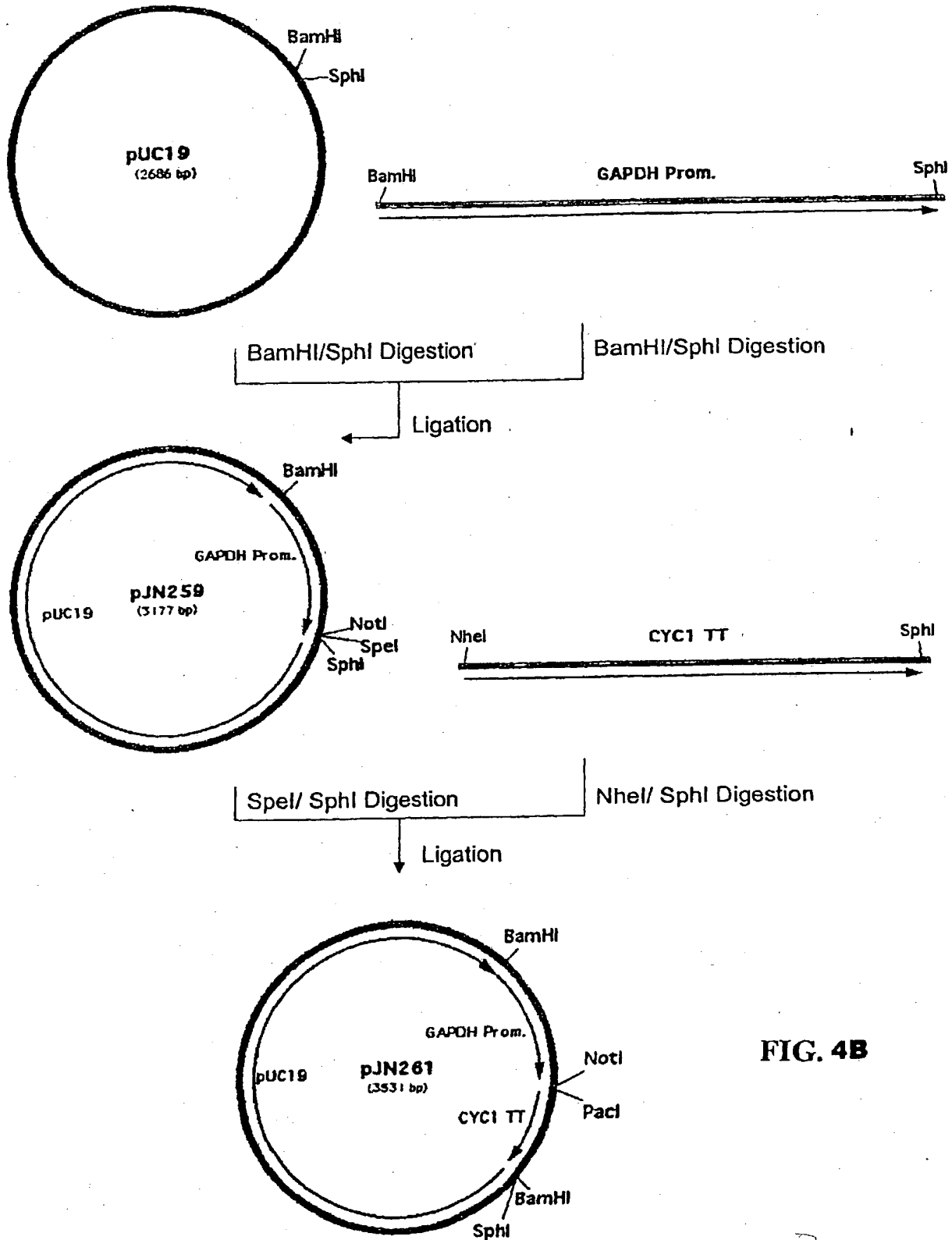


FIG. 4B

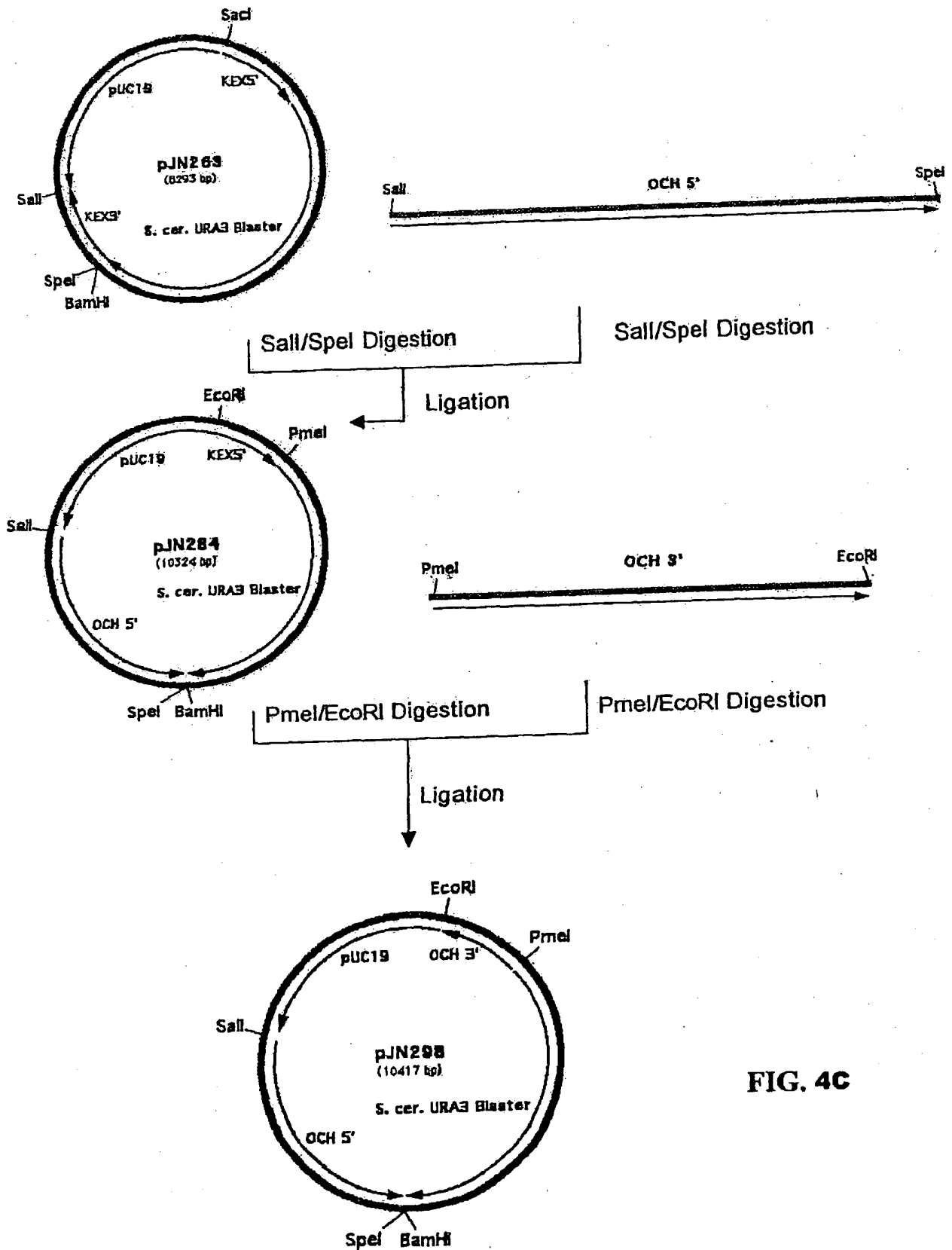


FIG. 4C

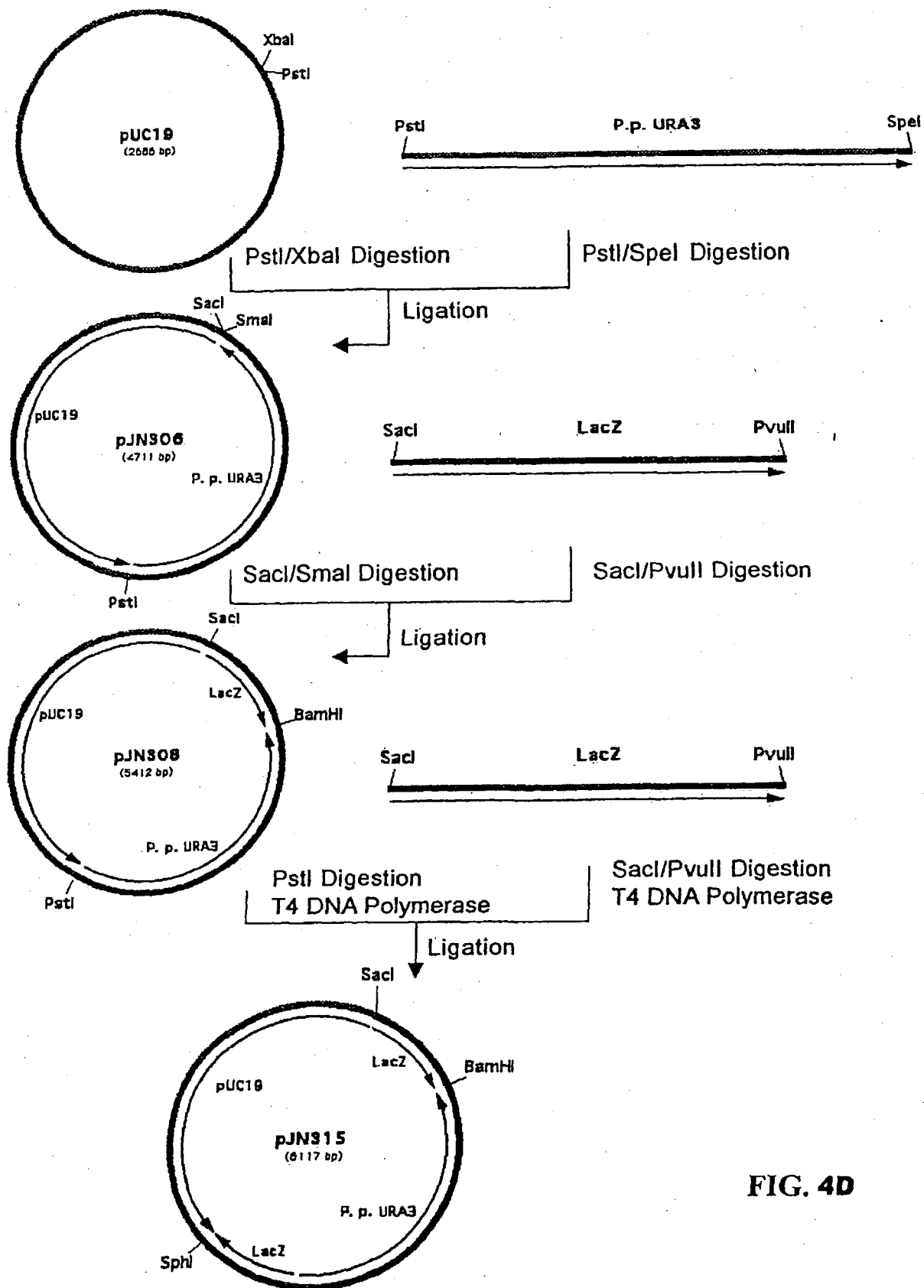


FIG. 4D

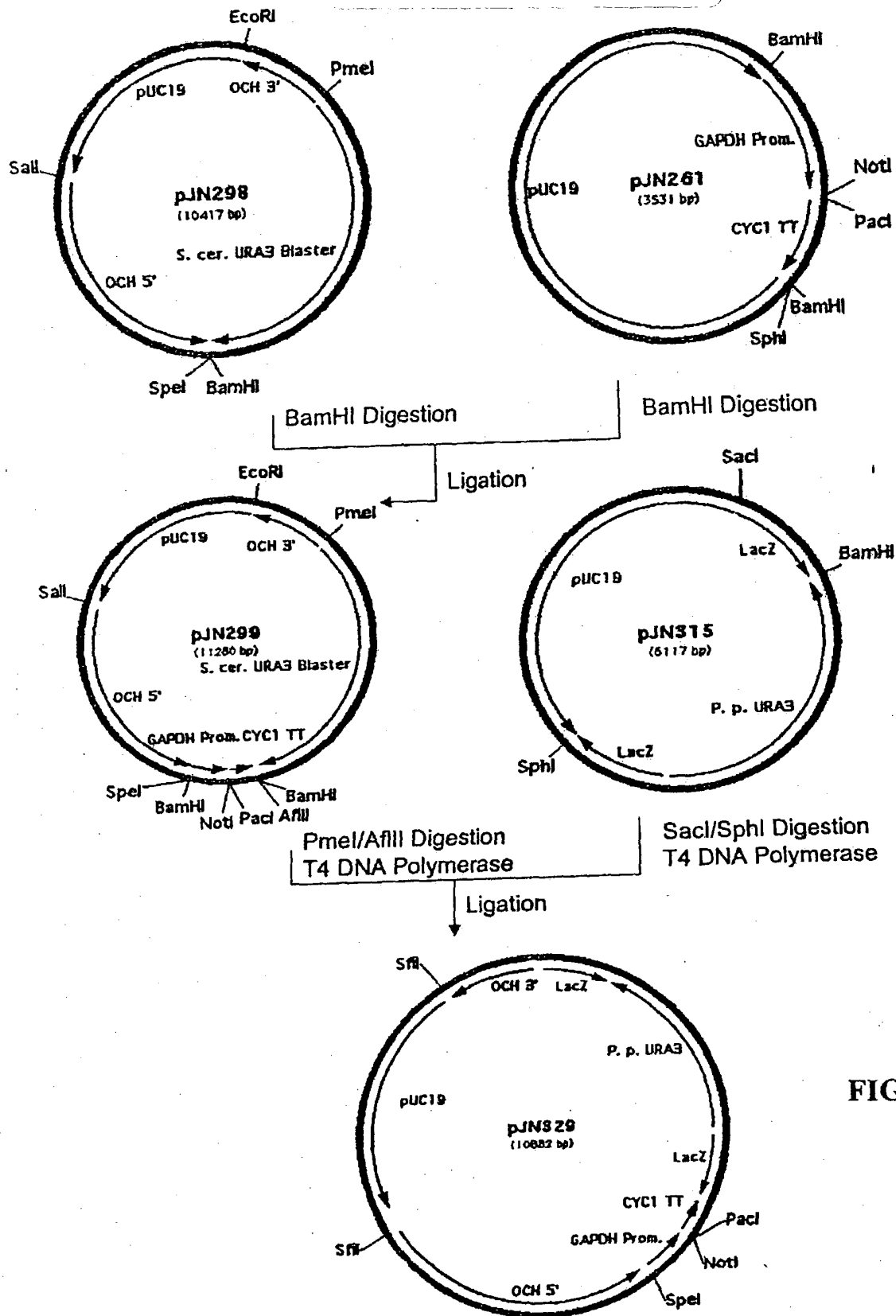


FIG. 4E

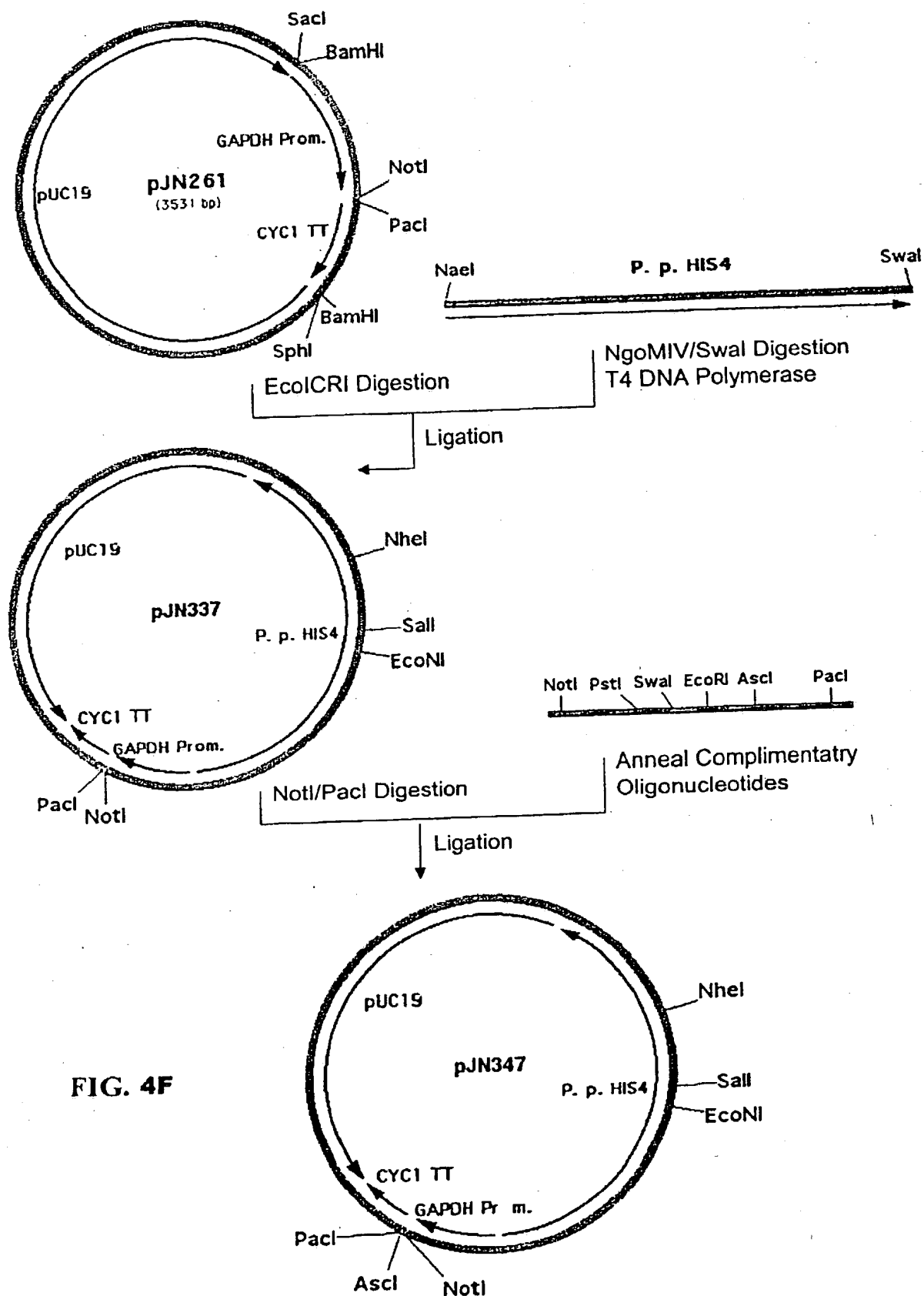


FIG. 4F

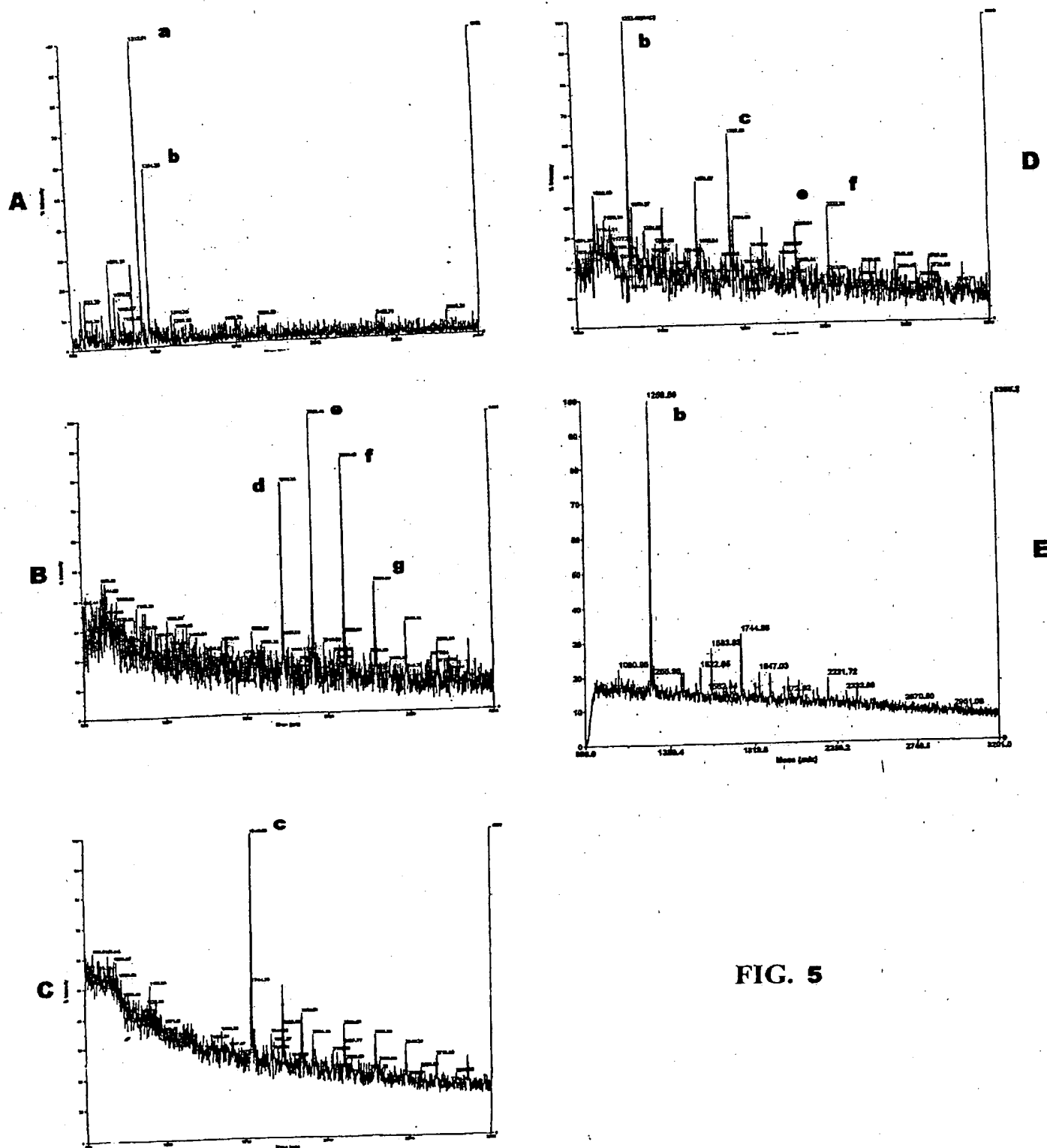
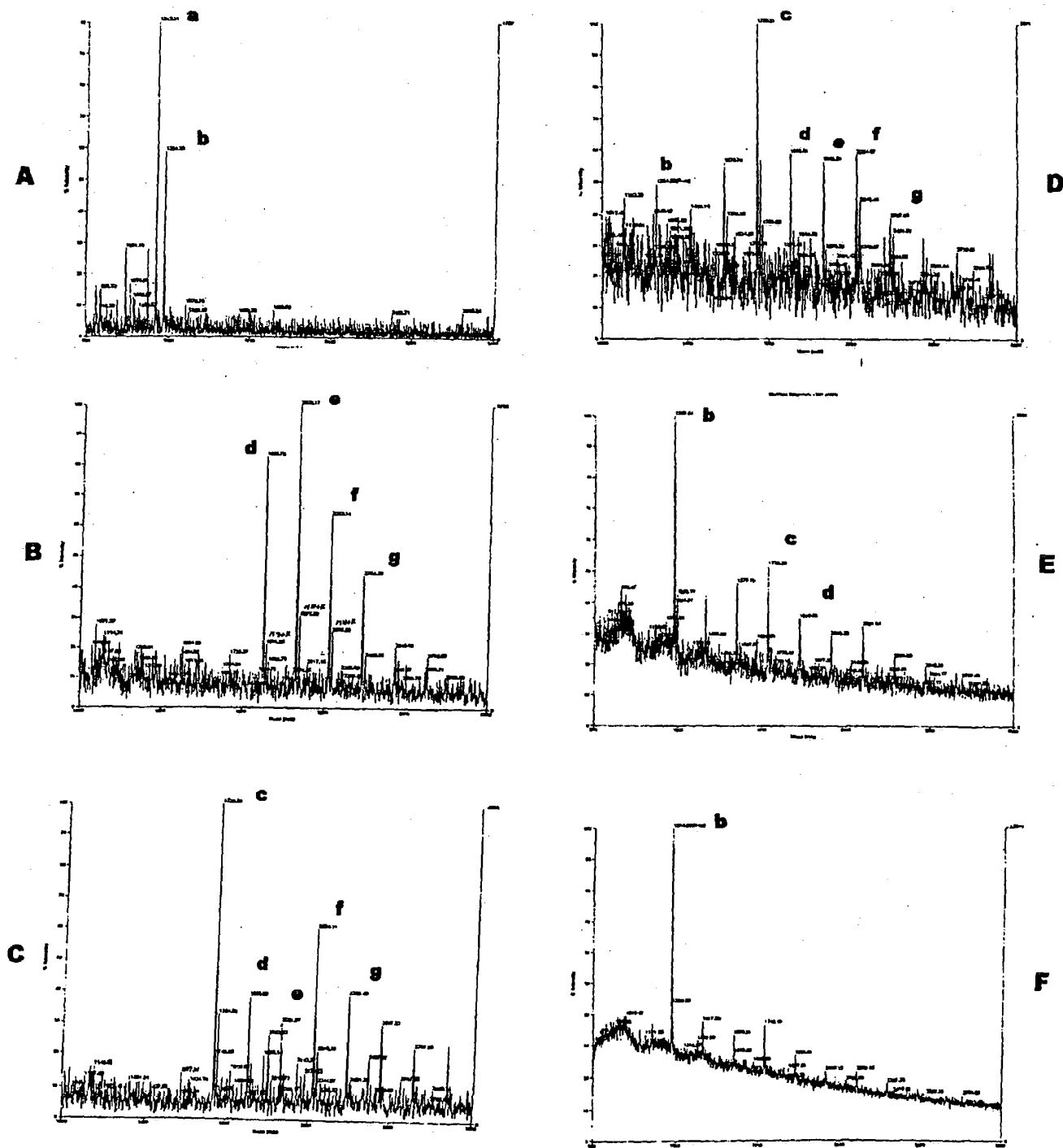
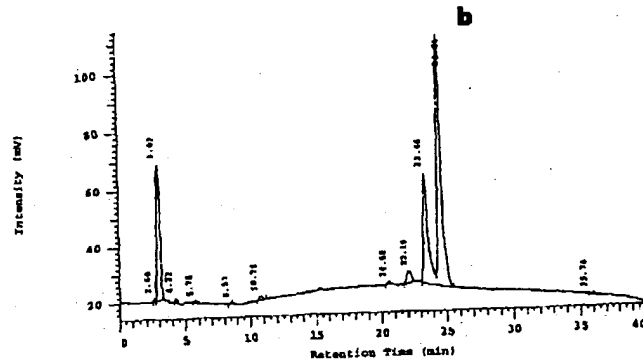


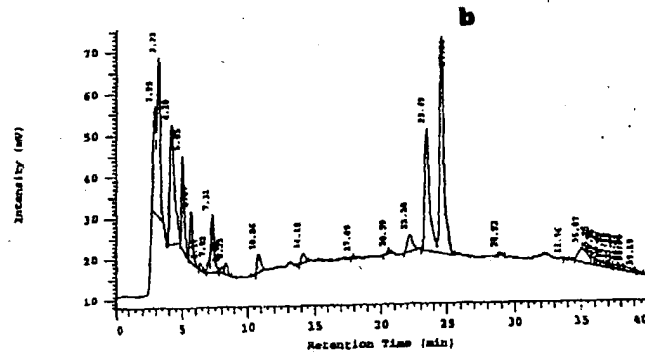
FIG. 6



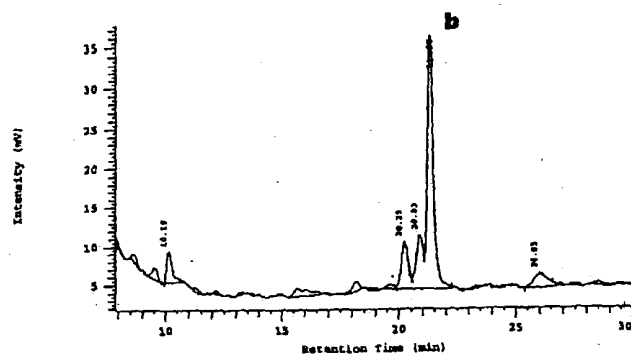
A



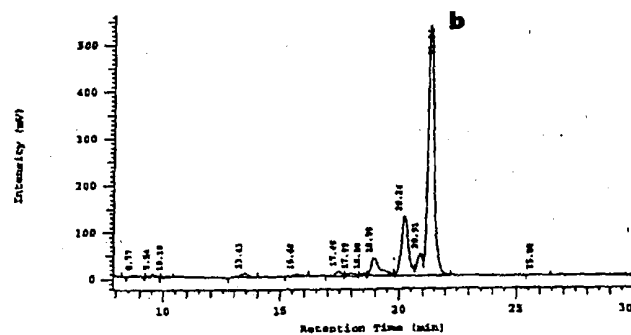
B



A



B



C

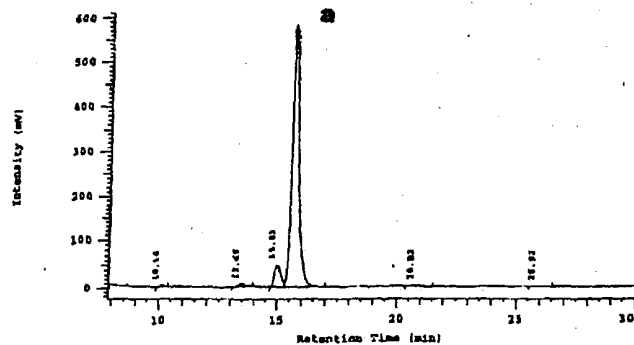
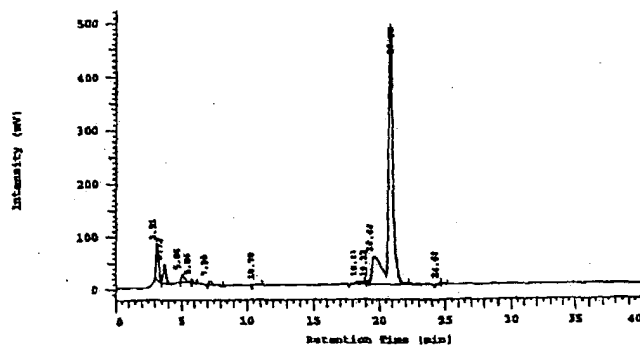
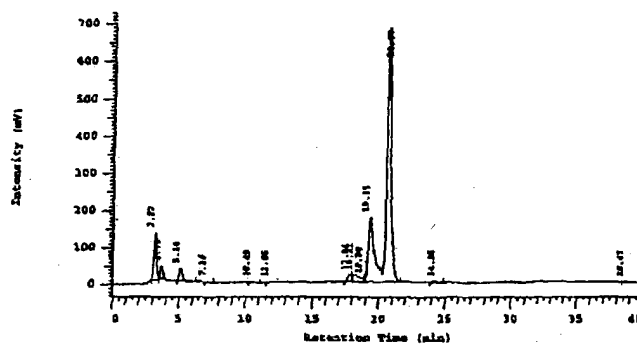


FIG. 8

A



B



C

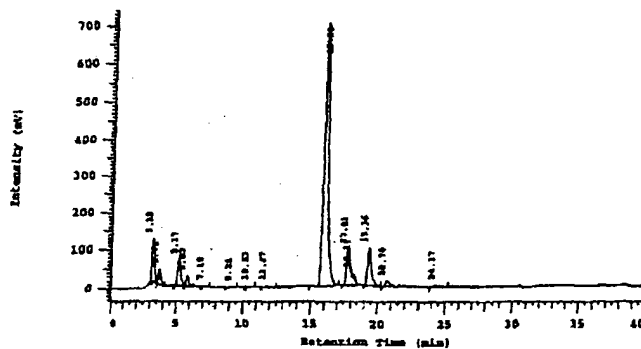
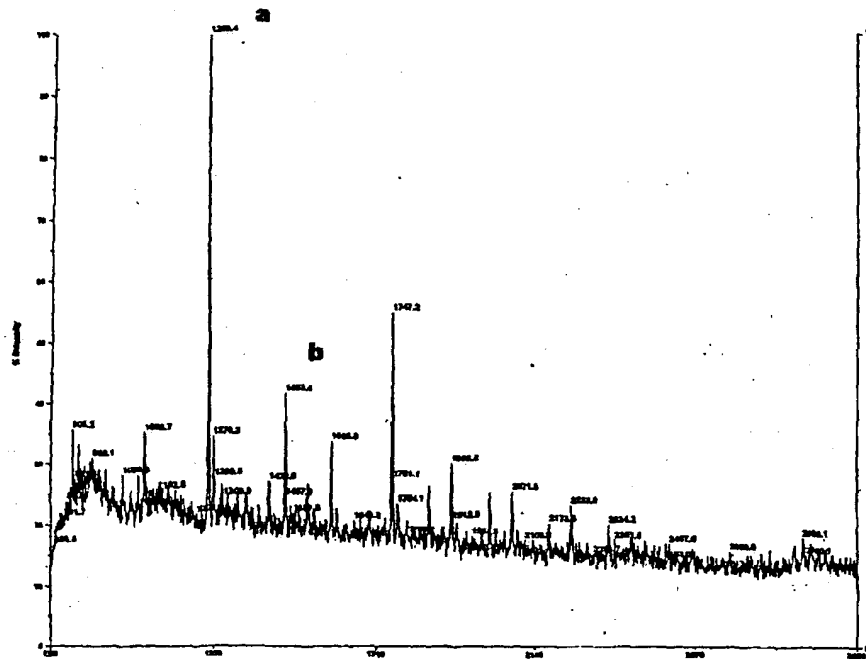


FIG. 9

FIG. 10



pH optimum for BB27-2 medium
C. elegans Mann1B D31 and S. Mnn10-s

pH	% of Man5
4.5	0
5	32
5.5	41
6	35
6.43	22
6.5	4
7.5	0
8.5	0

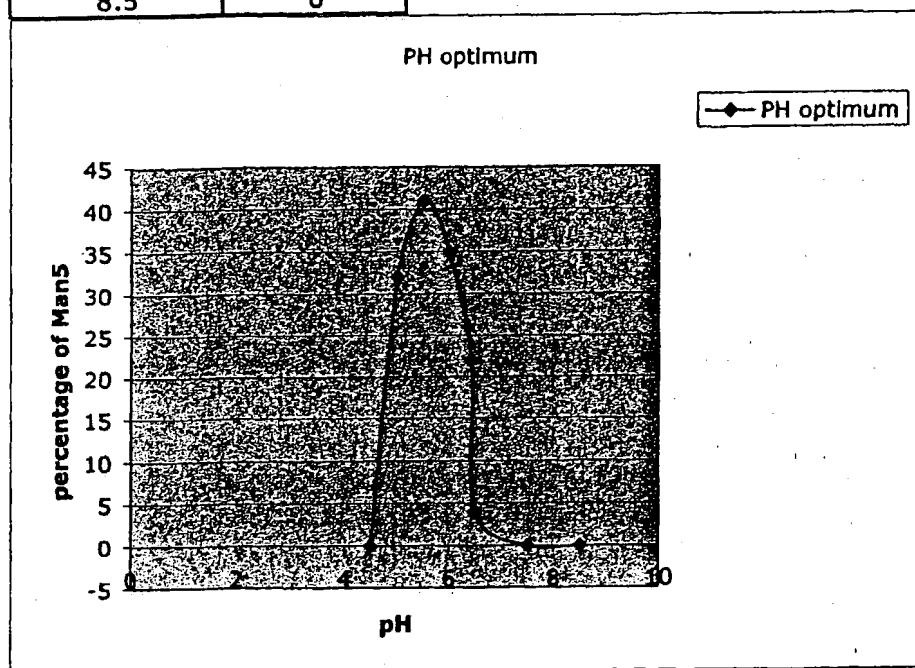
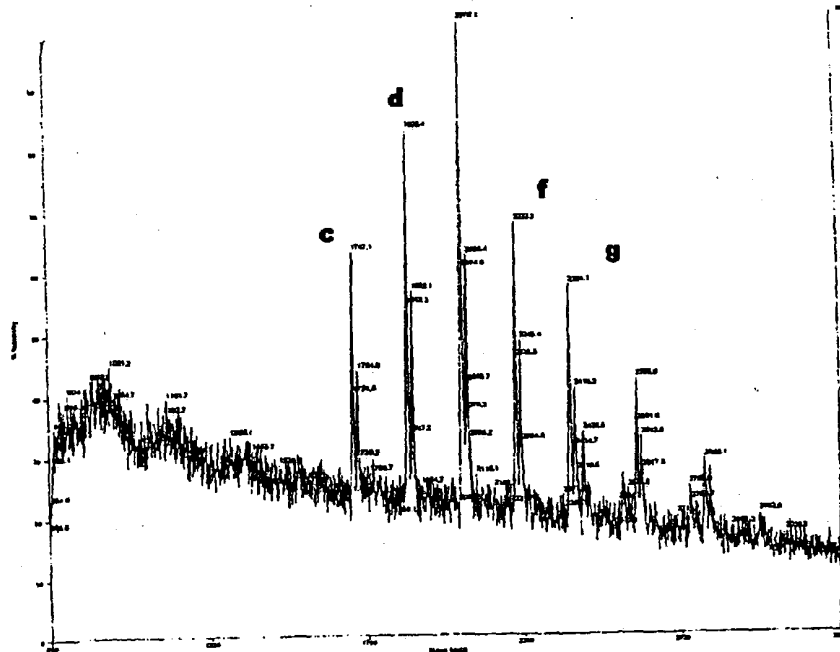
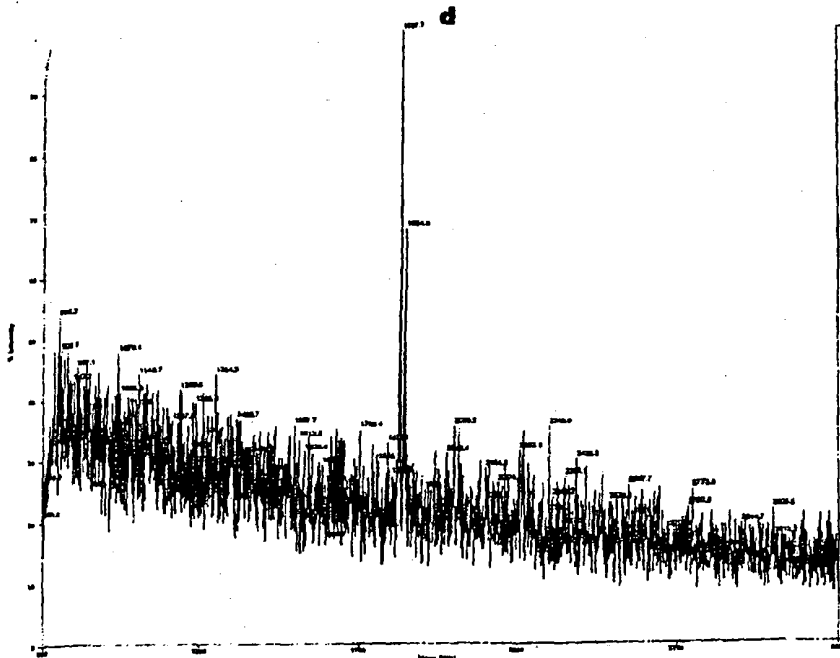


FIG. 11



A

FIG. 12



B

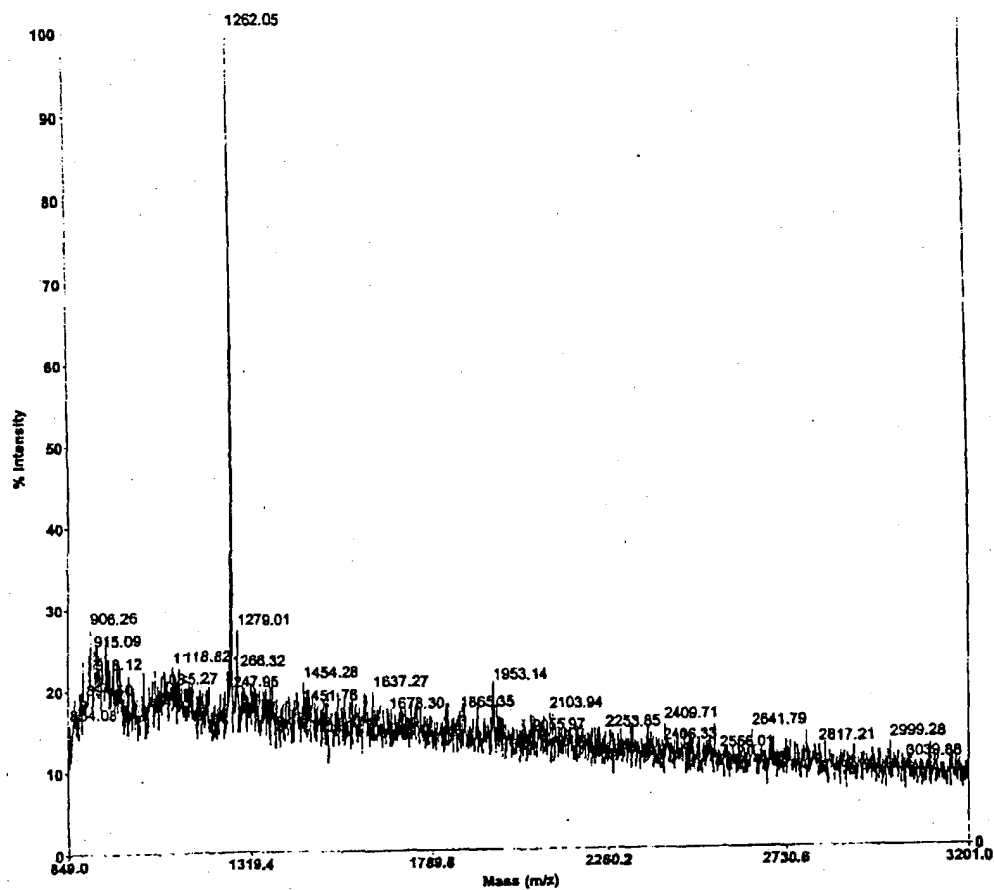


FIG. 12C

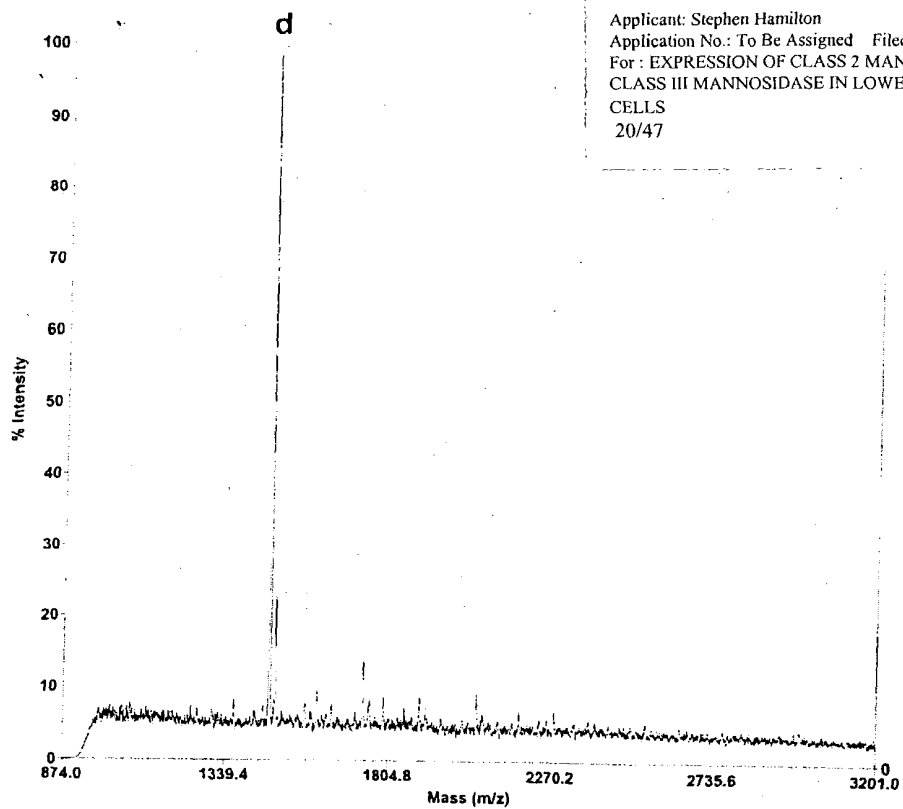


FIG. 13

Applicant: Stephen Hamilton GFI-107
Application No.: To Be Assigned Filed: Herewith
For: EXPRESSION OF CLASS 2 MANNOSIDASE AND
CLASS III MANNOSIDASE IN LOWER EUKARYOTIC
CELLS
21/47

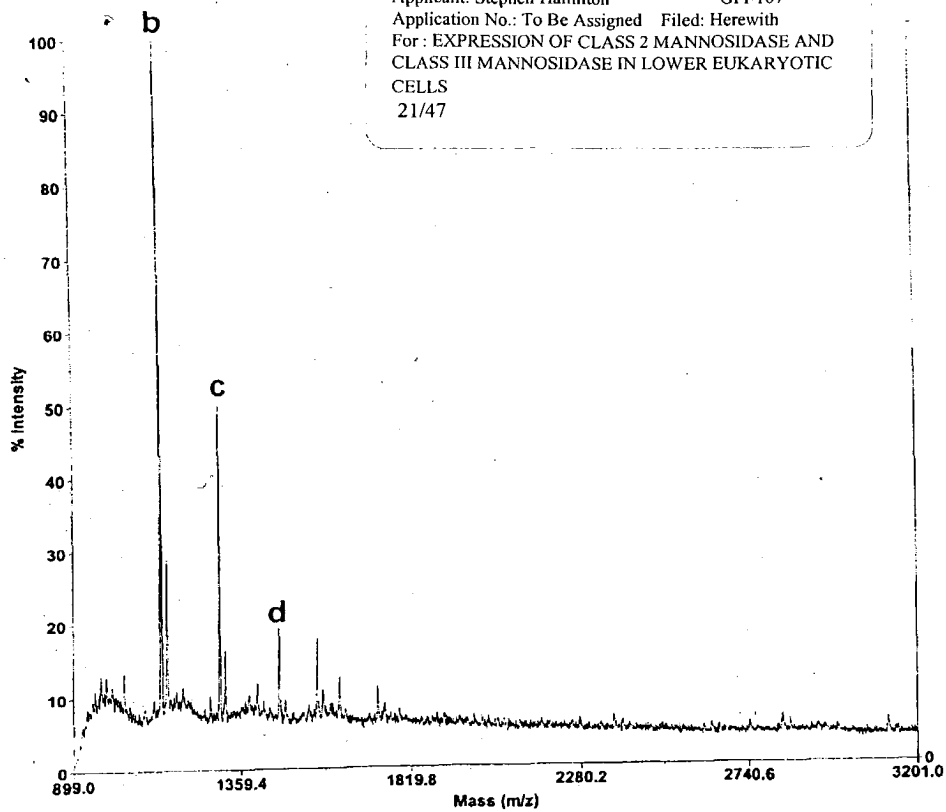


FIG. 14

Applicant: Stephen Hamilton GFI-107
Application No.: To Be Assigned Filed: Herewith
For: EXPRESSION OF CLASS 2 MANNOSIDASE AND
CLASS III MANNOSIDASE IN LOWER EUKARYOTIC
CELLS
22/47

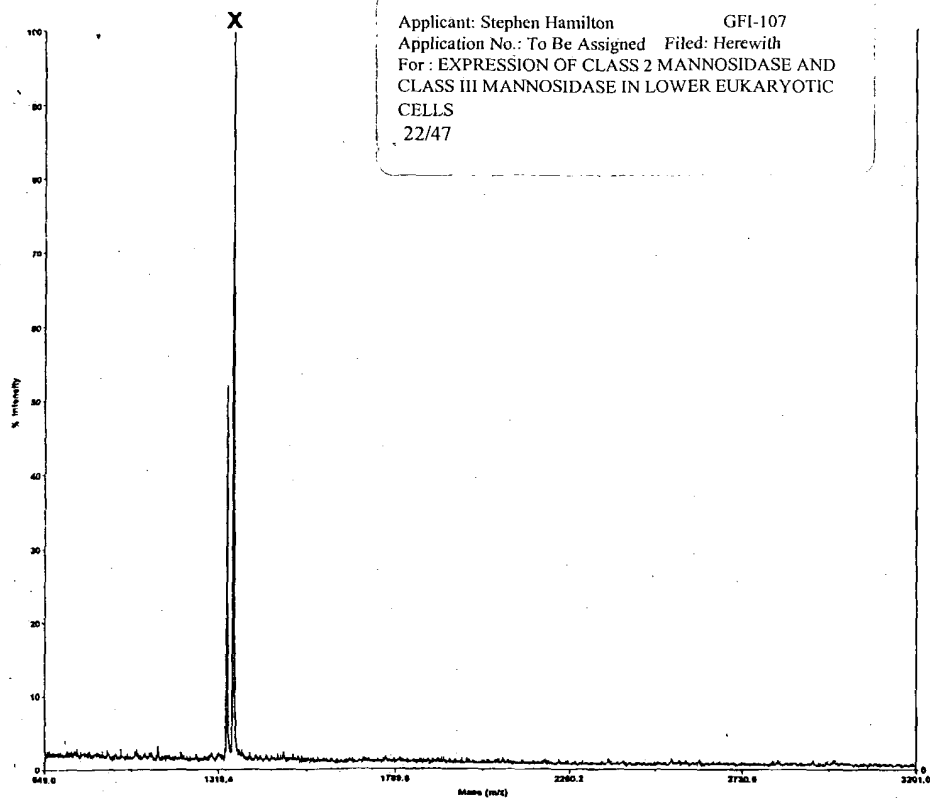


FIG. 15

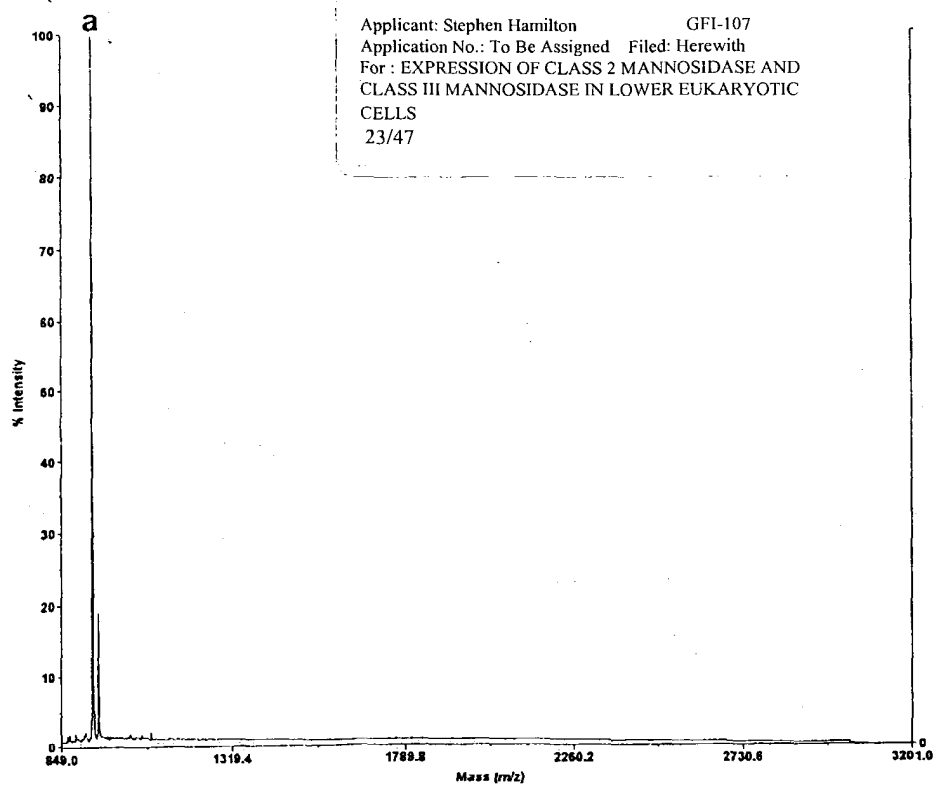


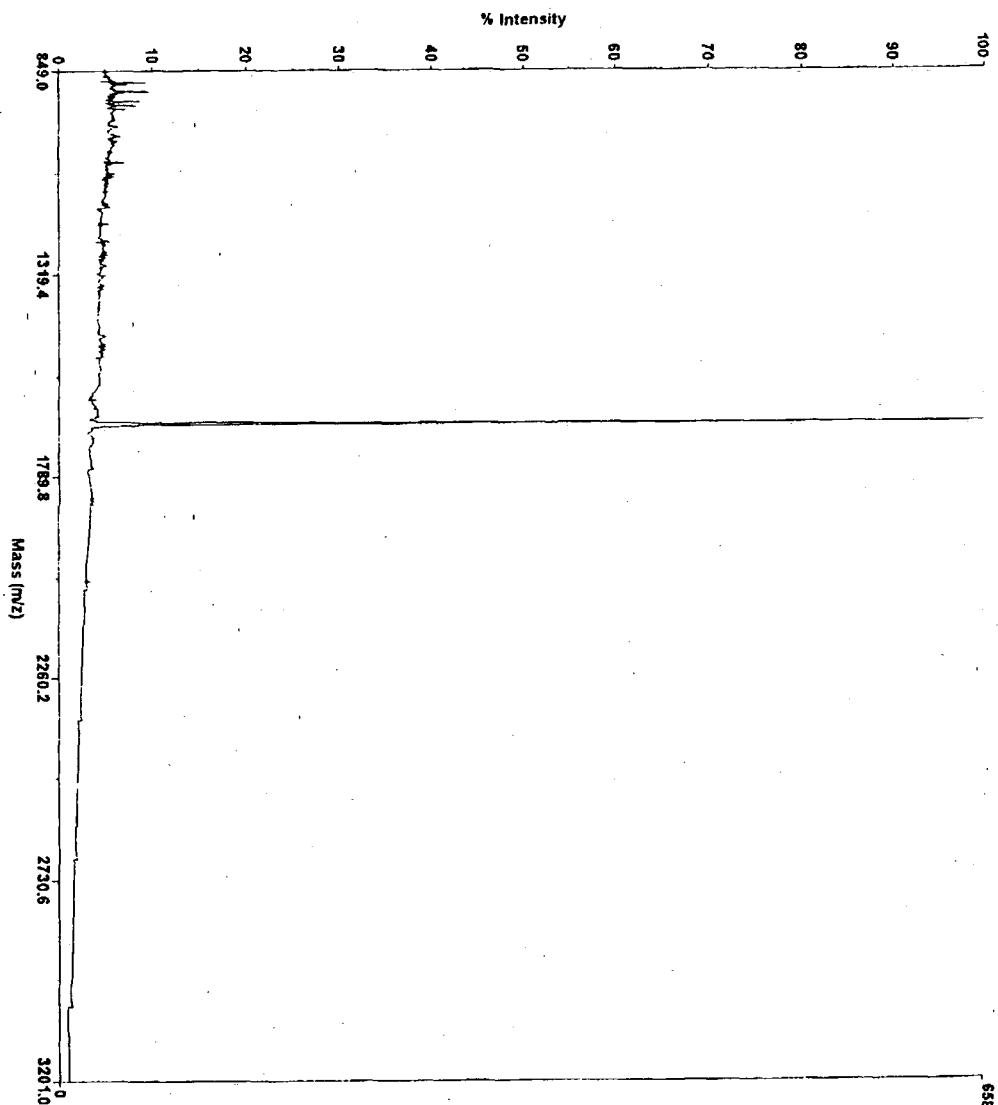
FIG. 16

Applicant: Stephen Hamilton
 Application No.: To Be Assigned Filed: Herewith
 For: EXPRESSION OF CLASS 2 MANNOSIDASE AND
 CLASS III MANNOSIDASE IN LOWER EUKARYOTIC
 CELLS
 24/47

FIG. 17

Applied Biosystems Voyager System 1246

Voyager Spec #1=>BC=>NR(2.00)[BP = 1664.6, 658]



Acquired: 10:12:00, June 13, 2003
 D:\GLVCO-F1\DATA\Wuhan Data\Other samples\June 2003\HL_6-13-03 Gal Transfer\6-2-03 SH MIV GN2M3 + GalT Sol_0001.dai

Mode of operation: Linear
 Extraction mode: Delayed
 Polarity: Positive
 Acquisition control: Manual
 Accelerating voltage: 20000 V
 Grid voltage: 94%
 Guide wire D: 0.05%
 Extraction delay time: 100 msec
 Acquisition mass range: 850 - 3200 Da
 Number of laser shots: 100/spectrum
 Laser intensity: 2713
 Laser Rep Rate: 20.0 Hz
 Calibration type: Default
 Calibration matrix: 2,5-Dihydroxybenzoic acid
 Low mass gate: 800 Da
 Digitizer start time: 18.582
 Bin size: 2 msec
 Number of data points: 8676
 Vertical scale: 500 mV
 Vertical offset: 0%
 Input bandwidth: 150 MHz
 Sample well: 47
 Plate ID: 100 WELL PLATE
 Serial number: 1246
 Instrument name: Voyager-DE
 Plate type filename: C:\VOYAGER\100 well plate.p
 Lab name: PE Biosystems
 Absolute x-position: 31305.6
 Absolute y-position: 28088.3
 Relative x-position: -761.973
 Relative y-position: 1081.83
 Shot in spectrum: 100
 Source pressure: 4.339e-007
 Mirror pressure: 0
 TC2 pressure: 0.004253
 TIS gate width: 30
 TIS flight length: 940

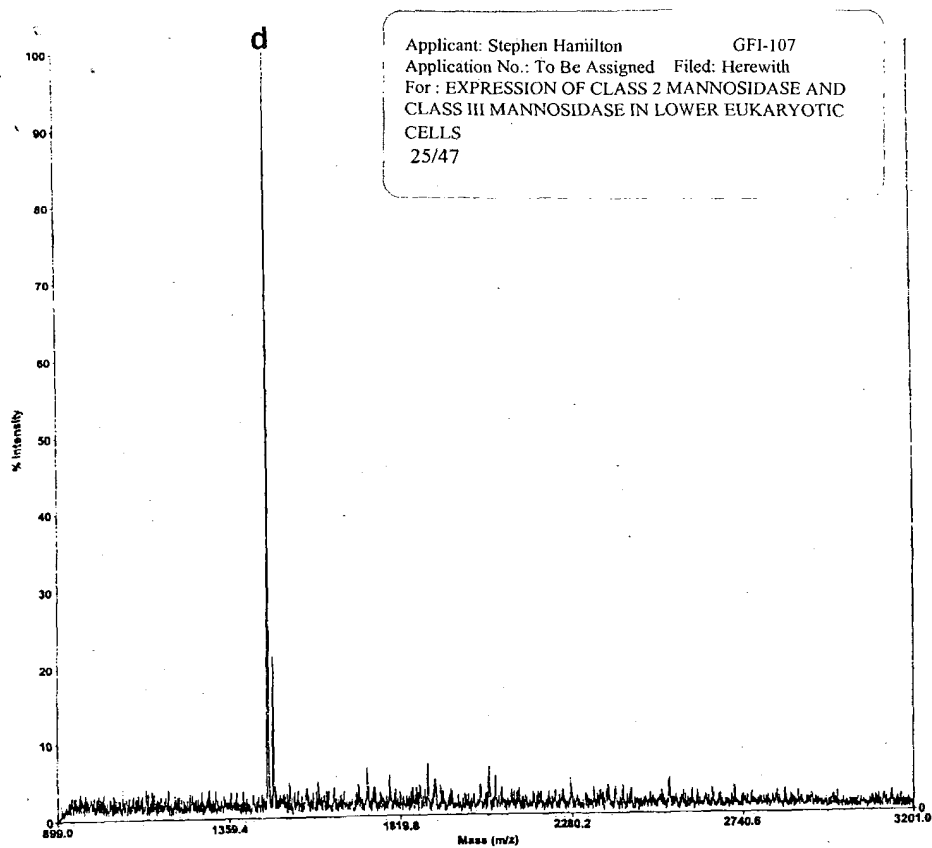


FIG. 18

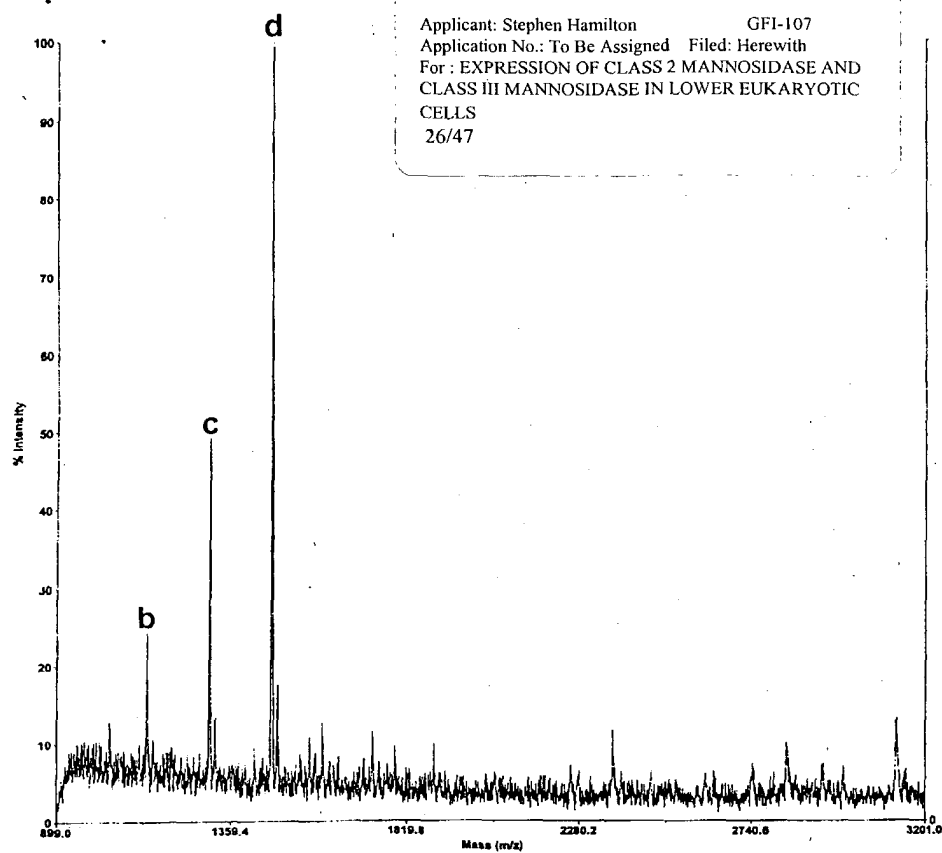


FIG. 19

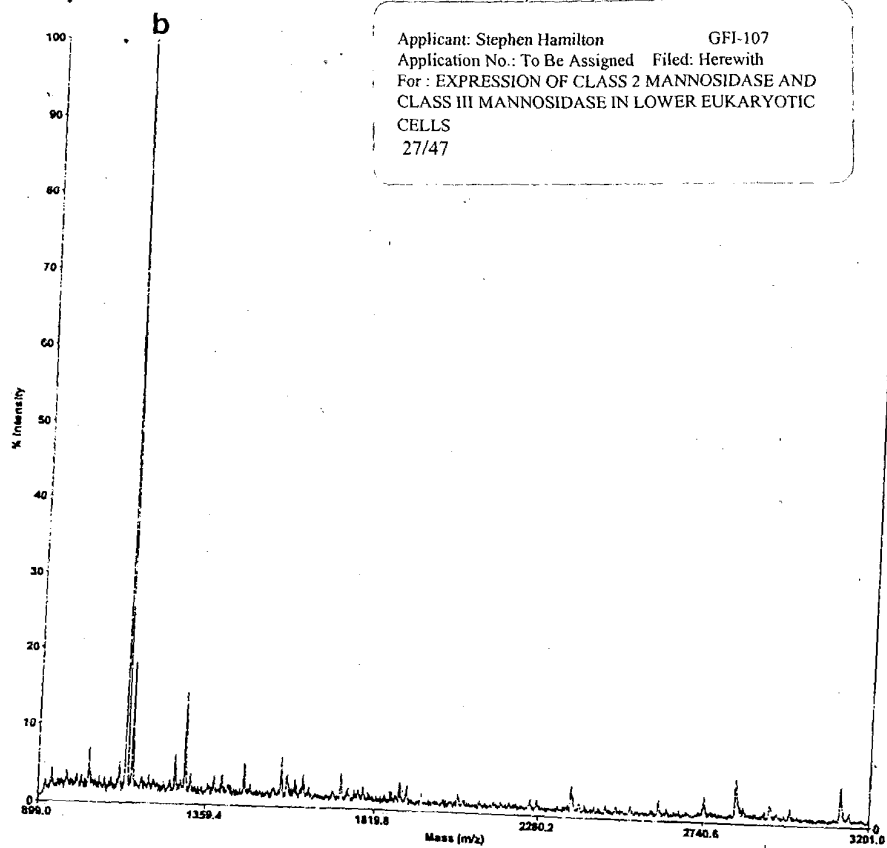


FIG. 20

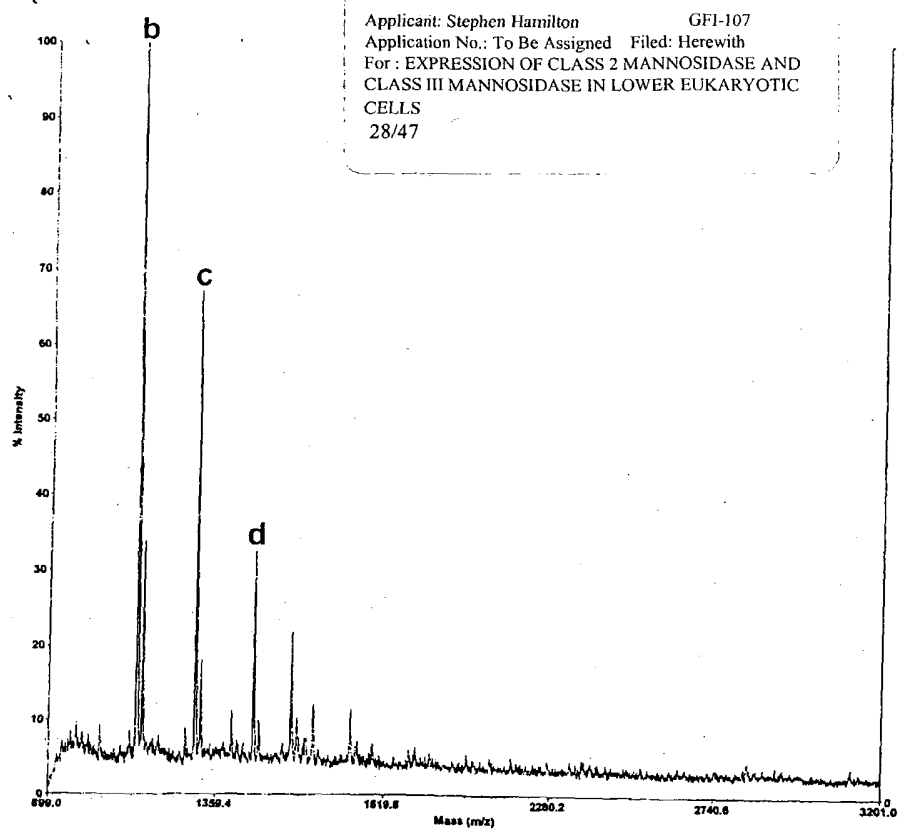


FIG. 21

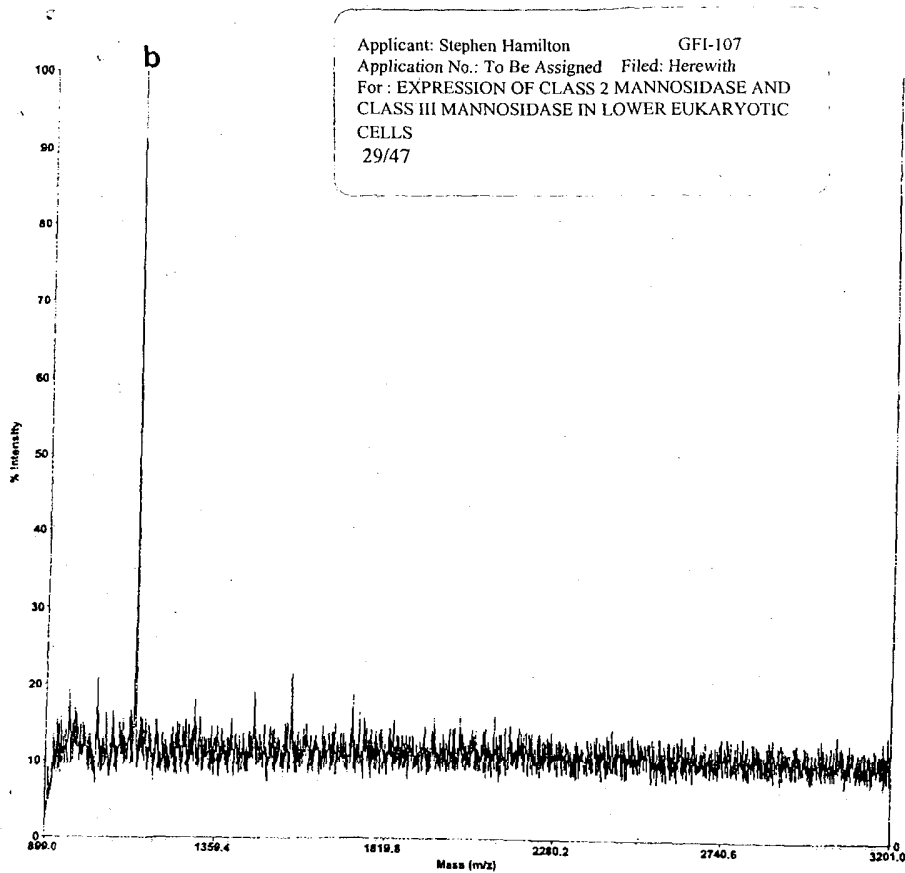


FIG. 22

Biology WorkBench

click here to
toggle between
menus and buttons

WE
Moved! <http://workbench.sdsc.edu/>

Version 3.2

BOXSHADE

Color-Coded Plots of Pre-Aligned Sequences

Selected Sequence(s)

- Droso MannII (X77652),
C.elegans MannII,
rMannII (XM_218816.1),
hMannIIx D55649,
Mouse MannII (X61172),
human MannII (U31520),
CionaMannII (AK116684),
ArabMannII,
Insect ManIII,
hLyso MannII,
hCyto MannII (NM_006715)

[Return](#) [Help](#) [Report Bugs](#)

Download a PostScript version of the output

```

Droso_MannII_[X 1 -----
C.elegans_MannI 1 -----
rMannII_[XM_218 1 MACIGGAGGQGRQAVERRIPSHQGYPMRWMTNGSCSEHALLSKTRMYCHQGCVRPPETDVKN
hMannIIa_D55649 1 -----
Mouse_MannII_[X 1 -----
hMannII 1 -----
CionaMannII_[AR 1 -----
ArabMannII 1 -----
Insect_MannIII 1 -----
hLyso_MannII 1 -----
hCyto_MannII_[N 1 -----

Droso_MannII_[X 1 -----MSTTRRFAVICSGCLVFLSLTILNFAAP-----AATQIRP
C.elegans_MannI 1 -----MGRLEYILCLG-VFLTVSLIYNGIETG-----ARALTKR
rMannII_[XM_218 61 PFTTTDTQSVPGVSTLRVNTCCGAATPCATPSLIMIDRVQHDPAR-HQNGCNPPRS
hMannIIa_D55649 1 -----LRLVNTCCGAATPCATPSLIMIDRVQHDPTTR-HQNGCNPPRS
Mouse_MannII_[X 1 -----LRLVNTCCGAATPCATPSLIMIDRGHLDYPRGPRQSGSFPOG
hMannII 1 -----LRLVNTCCGAATPCATPSLIMIDRGHLDYPRNPRRSGSFPOG
CionaMannII_[AR 1 -----LRLVNTCCGAATPCATPSLIMIDRGHLDYPRNPRRSGSFPOG
ArabMannII 1 -----LRLVNTCCGAATPCATPSLIMIDRGHLDYPRNPRRSGSFPOG
Insect_MannIII 1 -----LRLVNTCCGAATPCATPSLIMIDRGHLDYPRNPRRSGSFPOG
hLyso_MannII 1 -----LRLVNTCCGAATPCATPSLIMIDRGHLDYPRNPRRSGSFPOG
hCyto_MannII_[N 1 -----LRLVNTCCGAATPCATPSLIMIDRGHLDYPRNPRRSGSFPOG

Droso_MannII_[X 40 EYENEMRELENGHCHEGHEMREHARAKTNRD-----
C.elegans_MannI 37 CAYDURREGHLEVAENGRTIDRLEONORAKAKSVDFDEEHEKTRREHVEHEKRV
rMannII_[XM_218 120 QSVLONREOLECLREHREHISRDLSLEHANAEGPPALLPY-----
hMannIIa_D55649 46 QSVLONREOLECLREHREHISRDLSLEHANAEGPPALLPY-----
Mouse_MannII_[X 47 QSVLONREOLECLREHREHISRDLSLEHANAEGPPALLPY-----
hMannII 47 QSVLONREOLECLREHREHISRDLSLEHANAEGPPALLPY-----
CionaMannII_[AR 45 QSVLONREOLECLREHREHISRDLSLEHANAEGPPALLPY-----
ArabMannII 37 QSVLONREOLECLREHREHISRDLSLEHANAEGPPALLPY-----
Insect_MannIII 28 QSVLONREOLECLREHREHISRDLSLEHANAEGPPALLPY-----
hLyso_MannII 1 QSVLONREOLECLREHREHISRDLSLEHANAEGPPALLPY-----
hCyto_MannII_[N 34 QSVLONREOLECLREHREHISRDLSLEHANAEGPPALLPY-----

Droso_MannII_[X 77 -----DPIRPPLEVARSPRPGQCCQVVDVPHVQOMERATPRSPRDIE
C.elegans_MannI 97 APVPVRGHEGEMARHQVQRIRPTPSMDVCGIRENVSIARSDOMIDATTPRSPRDIE
rMannII_[XM_218 166 HTANGSAVLPEPRPEPPVSPEDQFALGGRGQRPOMITISDEPPDHV
hMannIIa_D55649 92 YTVGSMVVPPEPRPSPFFGISPODQFALGGRGQRPOMITISDEPPDHV
Mouse_MannII_[X 93 YTVGSMVVPPEPRPSPFFGISPODQFALGGRGQRPOMITISDEPPDHV
hMannII 93 YTVGSMVVPPEPRPSPFFGISPODQFALGGRGQRPOMITISDEPPDHV
CionaMannII_[AR 94 YTVGSMVVPPEPRPSPFFGISPODQFALGGRGQRPOMITISDEPPDHV
ArabMannII 83 YTVGSMVVPPEPRPSPFFGISPODQFALGGRGQRPOMITISDEPPDHV
Insect_MannIII 63 YTVGSMVVPPEPRPSPFFGISPODQFALGGRGQRPOMITISDEPPDHV
hLyso_MannII 13 YTVGSMVVPPEPRPSPFFGISPODQFALGGRGQRPOMITISDEPPDHV
hCyto_MannII_[N 71 YTVGSMVVPPEPRPSPFFGISPODQFALGGRGQRPOMITISDEPPDHV

Droso_MannII_[X 122 GGVNRGQVLEPLKNAHREDAVVPVPSHNTPE-----
C.elegans_MannI 157 GGVNRGQVLEPLKNAHREDAVVPVPSHNTPE-----
rMannII_[XM_218 219 GGVNRGQVLEPLKNAHREDAVVPVPSHNTPE-----
hMannIIa_D55649 145 GGVNRGQVLEPLKNAHREDAVVPVPSHNTPE-----
Mouse_MannII_[X 144 GGVNRGQVLEPLKNAHREDAVVPVPSHNTPE-----
hMannII 145 GGVNRGQVLEPLKNAHREDAVVPVPSHNTPE-----
CionaMannII_[AR 147 GGVNRGQVLEPLKNAHREDAVVPVPSHNTPE-----
ArabMannII 132 GGVNRGQVLEPLKNAHREDAVVPVPSHNTPE-----
Insect_MannIII 101 GGVNRGQVLEPLKNAHREDAVVPVPSHNTPE-----
hLyso_MannII 48 GGVNRGQVLEPLKNAHREDAVVPVPSHNTPE-----
hCyto_MannII_[N 107 GGVNRGQVLEPLKNAHREDAVVPVPSHNTPE-----

Droso_MannII_[X 162 FERTYQ-----HDKRHTSHARRHFERMFIWAEISFAERDGERLIG
C.elegans_MannI 197 FERTYQ-----HDKRHTSHARRHFERMFIWAEISFAERDGERLIG
rMannII_[XM_218 277 FERTYQ-----HDKRHTSHARRHFERMFIWAEISFAERDGERLIG
hMannIIa_D55649 184 FERTYQ-----HDKRHTSHARRHFERMFIWAEISFAERDGERLIG
Mouse_MannII_[X 183 FERTYQ-----HDKRHTSHARRHFERMFIWAEISFAERDGERLIG
hMannII 184 FERTYQ-----HDKRHTSHARRHFERMFIWAEISFAERDGERLIG
CionaMannII_[AR 186 FERTYQ-----HDKRHTSHARRHFERMFIWAEISFAERDGERLIG
ArabMannII 171 FERTYQ-----HDKRHTSHARRHFERMFIWAEISFAERDGERLIG
Insect_MannIII 142 FERTYQ-----HDKRHTSHARRHFERMFIWAEISFAERDGERLIG
hLyso_MannII 80 FERTYQ-----HDKRHTSHARRHFERMFIWAEISFAERDGERLIG
hCyto_MannII_[N 146 FERTYQ-----HDKRHTSHARRHFERMFIWAEISFAERDGERLIG

```

```
Droso_MammII_[X] 214 GYVAGG--LEVTSSVWIEANBYFA--COLIESQOLLEH--HETAGWAFOP
C.elegans_MammI 249 GYVAGG--LEVTSSVWIEANBYFA--COLIESQOLLEH--HETAGWAFOP
rMammII_[X]_218 329 HVGNGG--LEVTSSVWIEANBYFA--COLIESQOLLEH--HETAGWAFOP
hMammIIa_D55649 236 HVGNGG--LEVTSSVWIEANBYFA--COLIESQOLLEH--HETAGWAFOP
Mouse_MammII_[X] 235 HVGNGG--LEVTSSVWIEANBYFA--COLIESQOLLEH--HETAGWAFOP
hMammII 236 HVGNGG--LEVTSSVWIEANBYFA--COLIESQOLLEH--HETAGWAFOP
CionaMammII_[AR 238 HVGNGG--LEVTSSVWIEANBYFA--COLIESQOLLEH--HETAGWAFOP
ArabMammII 233 HVGNGG--LEVTSSVWIEANBYFA--COLIESQOLLEH--HETAGWAFOP
Insect_MamIII 194 HVGNGG--LEVTSSVWIEANBYFA--COLIESQOLLEH--HETAGWAFOP
hlyso_MammII 140 HVGNGG--LEVTSSVWIEANBYFA--COLIESQOLLEH--HETAGWAFOP
hCyto_MammII_[W 198 HVGNGG--LEVTSSVWIEANBYFA--COLIESQOLLEH--HETAGWAFOP

Droso_MammII_[X] 270 HSPSPK--LEVTSSVWIEANBYFA--COLIESQOLLEH--HETAGWAFOP
C.elegans_MammI 307 HSPSPK--LEVTSSVWIEANBYFA--COLIESQOLLEH--HETAGWAFOP
rMammII_[X]_218 375 HSPSPK--LEVTSSVWIEANBYFA--COLIESQOLLEH--HETAGWAFOP
hMammIIa_D55649 292 HSPSPK--LEVTSSVWIEANBYFA--COLIESQOLLEH--HETAGWAFOP
Mouse_MammII_[X] 291 HSPSPK--LEVTSSVWIEANBYFA--COLIESQOLLEH--HETAGWAFOP
hMammII 292 HSPSPK--LEVTSSVWIEANBYFA--COLIESQOLLEH--HETAGWAFOP
CionaMammII_[AR 294 HSPSPK--LEVTSSVWIEANBYFA--COLIESQOLLEH--HETAGWAFOP
ArabMammII 279 HSPSPK--LEVTSSVWIEANBYFA--COLIESQOLLEH--HETAGWAFOP
Insect_MamIII 250 HSPSPK--LEVTSSVWIEANBYFA--COLIESQOLLEH--HETAGWAFOP
hlyso_MammII 198 HSPSPK--LEVTSSVWIEANBYFA--COLIESQOLLEH--HETAGWAFOP
hCyto_MammII_[W 257 HSPSPK--LEVTSSVWIEANBYFA--COLIESQOLLEH--HETAGWAFOP

Droso_MammII_[X] 330 HSYDIPETCOGPRICCOFFR--G67GL6--HETAGWAFOP
C.elegans_MammI 367 HSYDIPETCOGPRICCOFFR--G67GL6--HETAGWAFOP
rMammII_[X]_218 435 HSYDIPETCOGPRICCOFFR--G67GL6--HETAGWAFOP
hMammIIa_D55649 352 HSYDIPETCOGPRICCOFFR--G67GL6--HETAGWAFOP
Mouse_MammII_[X] 351 HSYDIPETCOGPRICCOFFR--G67GL6--HETAGWAFOP
hMammII 352 HSYDIPETCOGPRICCOFFR--G67GL6--HETAGWAFOP
CionaMammII_[AR 354 HSYDIPETCOGPRICCOFFR--G67GL6--HETAGWAFOP
ArabMammII 339 HSYDIPETCOGPRICCOFFR--G67GL6--HETAGWAFOP
Insect_MamIII 309 HSYDIPETCOGPRICCOFFR--G67GL6--HETAGWAFOP
hlyso_MammII 252 HSYDIPETCOGPRICCOFFR--G67GL6--HETAGWAFOP
hCyto_MammII_[W 313 HSYDIPETCOGPRICCOFFR--G67GL6--HETAGWAFOP

Droso_MammII_[X] 389 AKLSEVLLPGLDGF--HETAGWAFOP
C.elegans_MammI 426 AKLSEVLLPGLDGF--HETAGWAFOP
rMammII_[X]_218 494 AKLSEVLLPGLDGF--HETAGWAFOP
hMammIIa_D55649 411 AKLSEVLLPGLDGF--HETAGWAFOP
Mouse_MammII_[X] 410 AKLSEVLLPGLDGF--HETAGWAFOP
hMammII 411 AKLSEVLLPGLDGF--HETAGWAFOP
CionaMammII_[AR 413 AKLSEVLLPGLDGF--HETAGWAFOP
ArabMammII 399 AKLSEVLLPGLDGF--HETAGWAFOP
Insect_MamIII 366 AKLSEVLLPGLDGF--HETAGWAFOP
hlyso_MammII 303 AKLSEVLLPGLDGF--HETAGWAFOP
hCyto_MammII_[W 373 AKLSEVLLPGLDGF--HETAGWAFOP

Droso_MammII_[X] 448 HDAERAG--HETAGWAFOP
C.elegans_MammI 485 HDAERAG--HETAGWAFOP
rMammII_[X]_218 553 HDAERAG--HETAGWAFOP
hMammIIa_D55649 470 HDAERAG--HETAGWAFOP
Mouse_MammII_[X] 469 HDAERAG--HETAGWAFOP
hMammII 470 HDAERAG--HETAGWAFOP
CionaMammII_[AR 472 HDAERAG--HETAGWAFOP
ArabMammII 458 HDAERAG--HETAGWAFOP
Insect_MamIII 426 HDAERAG--HETAGWAFOP
hlyso_MammII 361 HDAERAG--HETAGWAFOP
hCyto_MammII_[W 433 HDAERAG--HETAGWAFOP

Droso_MammII_[X] 492 HVEVMDYR--HETAGWAFOP
C.elegans_MammI 529 HVEVMDYR--HETAGWAFOP
rMammII_[X]_218 601 HVEVMDYR--HETAGWAFOP
hMammIIa_D55649 518 HVEVMDYR--HETAGWAFOP
Mouse_MammII_[X] 517 HVEVMDYR--HETAGWAFOP
hMammII 518 HVEVMDYR--HETAGWAFOP
CionaMammII_[AR 515 HVEVMDYR--HETAGWAFOP
ArabMammII 514 HVEVMDYR--HETAGWAFOP
Insect_MamIII 470 HVEVMDYR--HETAGWAFOP
hlyso_MammII 401 HVEVMDYR--HETAGWAFOP
hCyto_MammII_[W 474 HVEVMDYR--HETAGWAFOP

Droso_MammII_[X] 537 HGTARTEVVDYEC--HETAGWAFOP
C.elegans_MammI 578 HGTARTEVVDYEC--HETAGWAFOP
rMammII_[X]_218 655 HGTARTEVVDYEC--HETAGWAFOP
hMammIIa_D55649 572 HGTARTEVVDYEC--HETAGWAFOP
Mouse_MammII_[X] 571 HGTARTEVVDYEC--HETAGWAFOP
hMammII 572 HGTARTEVVDYEC--HETAGWAFOP
CionaMammII_[AR 569 HGTARTEVVDYEC--HETAGWAFOP
ArabMammII 567 HGTARTEVVDYEC--HETAGWAFOP
Insect_MamIII 530 HGTARTEVVDYEC--HETAGWAFOP
hlyso_MammII 448 HGTARTEVVDYEC--HETAGWAFOP
hCyto_MammII_[W 523 HGTARTEVVDYEC--HETAGWAFOP

Droso_MammII_[X] 594 HPGGGHDS--HETAGWAFOP
C.elegans_MammI 628 HPGGGHDS--HETAGWAFOP
```


33/47

Biology WorkBench 3.2 - BOXSHADE

6/3/03 3:15

```

rMannII_DCM_218 715 GGGST-HPGAALVPAASAAALPQR-APRTAVYDHLI-CELESLV-ALIPSPRVE-SEN
bMannIIa_D55649 630 LGRDA P-----ERTVQLDG-EPPTV-AMPLI-CELESLV-ALIPSPRVE-SEN
Mouse_MannII_[X 629 SSGOS P-----QRILQLSAGEPIY-AMPLI-CELESLV-ALIPSPRVE-SEN
hMannII 630 KSGOS P-----QWIRISA-EPPTV-AMPLI-CELESLV-ALIPSPRVE-SEN
CionaMannII_[AK 626 QWQOPAP-----VVVLTPTNEXA-AMPLI-CELESLV-ALIPSPRVE-SEN
ArabMannII 627 YDARP-ERP-----AAREGSGST-AMPLI-CELESLV-ALIPSPRVE-SEN
Insect_MannII 590 PER-----QVGFIDREK-AMPLI-CELESLV-ALIPSPRVE-SEN
hLyso_MannII 508 R-----FQVNDIGREVE-AMPLI-CELESLV-ALIPSPRVE-SEN
hCyto_MannII_[W 583 -----SCIONVABEA-CHED-RSHGNT-AAAAALCAGPGPB

Droso_MannII_[X 645 H-HPTEAC-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
C.elegans_MannI 674 P-DIKCO-SEVIAXDNRITLVVNG-----I-CELESLV-ALIPSPRVE-SEN
rMannII_DCM_218 774 E-CP-IVG-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
bMannIIa_D55649 680 E-CP-IVG-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
Mouse_MannII_[X 680 E-CP-IVG-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
hMannII 680 E-CP-IVG-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
CionaMannII_[AK 677 E-CP-IVG-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
ArabMannII 676 W-TCVPS-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
Insect_MannII 633 KRRRLY-CP-IVG-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
hLyso_MannII 541 E-RTVPS-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
hCyto_MannII_[W 623 E-L-IVG-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN

Droso_MannII_[X 706 HTSYASLLLRKPTSLPLOC-PED-EPGDP-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
C.elegans_MannI 728 VEITENAAHFKETSPSSSTSGDPT-REDRV-ANF-ORNGM-KRATS-----LVDDP-DL
rMannII_DCM_218 824 LQSGEVVYLYNGVLEVSRTTP-PA-DAGTS-PA-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
bMannIIa_D55649 730 LQSGEVVYLYNGVLEVSRTTP-PA-DAGTS-PA-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
Mouse_MannII_[X 730 LADYVLYNH-----GLAENGIV-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
hMannII 730 LADYVLYNH-----GLAENGIV-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
CionaMannII_[AK 727 TESTVPI-PRVGP-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
ArabMannII 727 ATPSLRYASEFDPP-CP-IVG-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
Insect_MannII 688 CVIFCHN-----CEYQK-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
hLyso_MannII 589 ABAPQ-----CP-IVG-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
hCyto_MannII_[W 674 QQ-----P-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN

Droso_MannII_[X 763 T-SPRVP-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
C.elegans_MannI 785 HSPFIRY-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
rMannII_DCM_218 881 V-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
bMannIIa_D55649 787 V-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
Mouse_MannII_[X 782 K-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
hMannII 781 K-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
CionaMannII_[AK 782 V-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
ArabMannII 781 H-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
Insect_MannII 738 K-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
hLyso_MannII 628 M-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
hCyto_MannII_[W 714 R-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN

Droso_MannII_[X 808 V-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
C.elegans_MannI 830 M-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
rMannII_DCM_218 927 L-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
bMannIIa_D55649 833 C-----V-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
Mouse_MannII_[X 828 V-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
hMannII 827 V-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
CionaMannII_[AK 829 V-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
ArabMannII 821 V-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
Insect_MannII 792 I-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
hLyso_MannII 678 H-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
hCyto_MannII_[W 759 R-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN

Droso_MannII_[X 852 V-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
C.elegans_MannI 879 R-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
rMannII_DCM_218 977 R-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
bMannIIa_D55649 874 R-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
Mouse_MannII_[X 878 R-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
hMannII 877 R-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
CionaMannII_[AK 882 R-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
ArabMannII 880 R-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
Insect_MannII 846 R-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
hLyso_MannII 727 R-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
hCyto_MannII_[W 814 R-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN

Droso_MannII_[X 902 R-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
C.elegans_MannI 929 R-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
rMannII_DCM_218 1027 R-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
bMannIIa_D55649 922 R-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
Mouse_MannII_[X 928 R-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
hMannII 927 R-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
CionaMannII_[AK 932 R-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
ArabMannII 930 R-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
Insect_MannII 898 R-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
hLyso_MannII 785 R-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
hCyto_MannII_[W 858 R-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN

Droso_MannII_[X 960 R-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
C.elegans_MannI 987 R-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
rMannII_DCM_218 1085 R-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN
bMannIIa_D55649 980 R-SEVCMHEDTLTKTIRPOGSTR-ETIAR-EP-CELESLV-ALIPSPRVE-SEN

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Mouse_MannII_[X 986 -----SPVSYPSISGNTSPTDREPLPTVSG
hMannII 985 -----S-VSYPSISGNTSPTDREPLPTVSG
CionaMannII_[AK 990 -----AKIAYPSISAVYQ65NHTDREPLPTVSG
ArabMannII 989 -----MPRPSISGNTSPTDREPLPTVSG
Insect_MannIII 956 -----SMPGSTRARDTSKPGFVNRFPQPGQNSPYQVSTADYLSNHTDREPLPTVSG
hLyso_MannII 843 -----VLDTAQAAAGHR-----IAEQETLASCVVADPG
hCyto_MannII_[W 916 -----QDAGVQAAYSLH-----HIALPAPSPAPATSWAFSS
Droso_MannII_[X 1000 -----NEWIGAGG-----PGGDEIAREDDISVRRITFS
C.elegans_MannI 1027 -----TPKISSK-----MORRICHITTPRASPTTY
rMannII_OCM_218 1126 -----RSTSEPTER-----SRPLASPPCPHLDLSPARVSVPRANPRROAEPCLIGRAAD
hMannIIa_D55649 1020 -----NQIPGPGK-----SRPLASPPCPHLDLSPARVSVPRANPRROAEPCLIGRAAD
Mouse_MannII_[X 1027 -----QIPSPATKLLSEPIQSSPPCPHLDLSPARVSVPRANPRROAEPCLIGRAAD
hMannII 1023 -----KYSSPTKLOGSPPIQSSPPCPHLDLSPARVSVPRANPRROAEPCLIGRAAD
CionaMannII_[AK 1032 -----PWHLEKESPPRPPCHHLDLSPARVSVPRANPRROAEPCLIGRAAD
ArabMannII 1029 -----PQDISVPPQYGSAPLAPRPPCHHLDLSPARVSVPRANPRROAEPCLIGRAAD
Insect_MannIII 1016 -----SEVGEIRK-----QSYLQSPFPGHLDLSPARVSVPRANPRROAEPCLIGRAAD
hLyso_MannII 875 -----GAAYNLGAPPRTPSGPRRDPSPHLDLSPARVSVPRANPRROAEPCLIGRAAD
hCyto_MannII_[W 953 -----PAVVLTK-----QATSPQRESVLELYEAE
Droso_MannII_[X 1032 -----SARTORVYCHERTNLAGCTPRERTQELDVCHLLPNVARCERTITYL
C.elegans_MannI 1059 -----KANKERTYERKAAVMKREVPCR-SRLTLPDTSCLATGLEIEP
rMannII_OCM_218 1183 -----PPPLLSLTVPQDTLPADLHNRPPCPHLDLSPARVSVPRANPRROAEPCLIGRAAD
hMannIIa_D55649 1056 -----DILPABTAHLNRPPCPHLDLSPARVSVPRANPRROAEPCLIGRAAD
Mouse_MannII_[X 1066 -----KGYDEALHLNRPPCPHLDLSPARVSVPRANPRROAEPCLIGRAAD
hMannII 1060 -----NGBNHVALHLNRPPCPHLDLSPARVSVPRANPRROAEPCLIGRAAD
CionaMannII_[AK 1064 -----VAPDQSAHLNRPPCPHLDLSPARVSVPRANPRROAEPCLIGRAAD
ArabMannII 1065 -----QOLEHDEPRFALNRPPCPHLDLSPARVSVPRANPRROAEPCLIGRAAD
Insect_MannIII 1052 -----LPPNRYVNRPPCPHLDLSPARVSVPRANPRROAEPCLIGRAAD
hLyso_MannII 916 -----LEQFAVERDSGRNLAPVTLNLDPSFTYIRLQTTTLVANGLERAA
hCyto_MannII_[W 981 -----GRVDCVHLNLPVCELCILERRDPAGHLTSGQPPHNLFS
Droso_MannII_[X 1081 -----CMRHLDGMAPEVCPME-----TAAYSG66
C.elegans_MannI 1107 -----STPKSARKSTNLYEGH-----KARQPRLOEMTISITISY
rMannII_OCM_218 1243 -----F-LPPSISLXPLASPS-----NSTDLSMEIISLILNG
hMannIIa_D55649 1103 -----F-LPPSISLXPLASPS-----NSTDLSMEIISLILNG
Mouse_MannII_[X 1112 -----S-LVPISLXMRSPDDAQ-----HNSLMSMEIISLILNG
hMannII 1108 -----S-LTPSISLXMRSPDDAQ-----HNSLMSMEIISLILNG
CionaMannII_[AK 1112 -----S-LRRSISLXMRSPDDAQ-----HNSLMSMEIISLILNG
ArabMannII 1119 -----SKRPPSHMLQDMEILGYDDQELPDSSQPRGRHNSLMSMEIISLILNG
Insect_MannIII 1100 -----LITGLRTPPTG-----LSDRMAEVEITRY
hLyso_MannII 965 -----SRKWRKSGPTPTPTPY-----QLDPANLMSMEIISLILNG
hCyto_MannII_[W 1027 -----SAPVARLASATLEPMG-----NGFVCRINGTISASPA
  
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Return Help Report Bugs

Citation

Algorithm Citation:

Not given, but presumably Kay Hofmann and Michael D. Baron.

Program Citation:

Boxshade version 3.3.1, by Kay Hofmann and Michael D. Baron.



FIG. 24

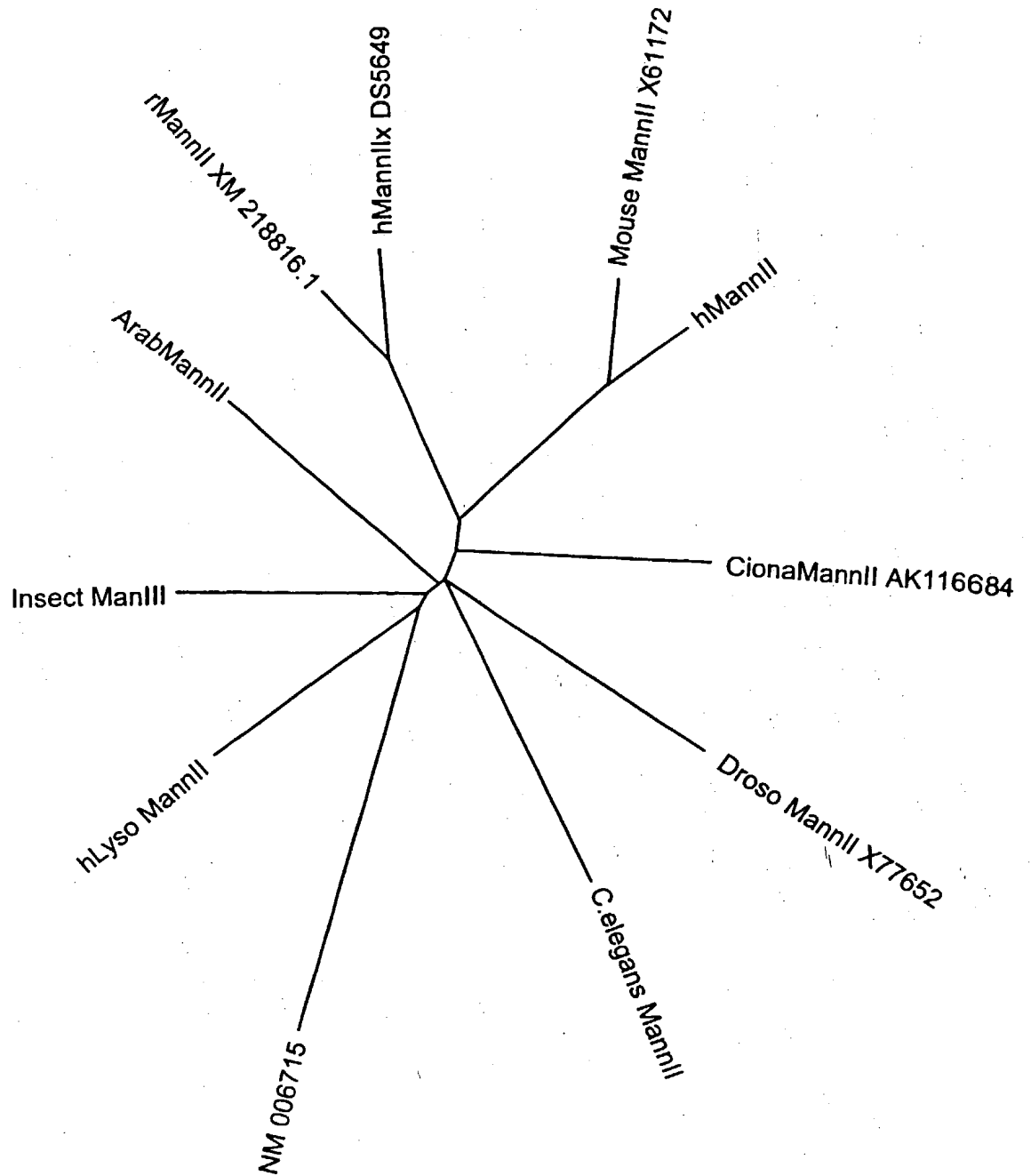


FIG. 25

Arabidopsis thaliana Mannosidase II (NM_121499)

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1 ATGCCGTTCTCTCGTATATCGGCAACAGCCGCGCTAGCTCCACCGCGGAGGAACCGCGGTTGGGGCCAATCTCTTCTTCCAACAGCGTTATCAAAGTCAAACTAG
110 M P F S S Y I G N S R R S S T G G G T G G W G Q S L L P T A L S K S K L
37 A I N R K P R K R T L V N F I F A N F F V I A L T V S L L F F L L T L F
219 CCAGTTCGGCGTACCAGGACCGATCTCTCAGGATTCCTTACCTCCAGATCCAAATCGGATCGTCAAGCCACGGAAGAATATTAAATCGCGACCCCTAAACGATTCCAAT
73 H F G V P G P I S S R F L T S R S N R I V K P R K N I N R R P L N D S N
328 TCAGCGCCCGCTCGTGTATATCACAACCTAAAGATCTATACGATAGGATTGAGTTTCTTGATACAGATGGTGGTCCATGGAAACAGGTTGGAGAGTTACGTATAAAGACG
110 S G A V V D I T T K D L Y D R I E F L D T D G G P W K Q G W R V T Y K D
437 ATGAGTGGGAGAAAGAGAAGCTCAAAATCTTCTGTTCTCTCATTAACGATCCTGGTGGAAATGACTGTAGAGGAGTATTATCAGAGACAATCCAGACATAT
146 D E W E K E K L K I F V V P H S H N D P G W K L T V E E Y Y Q R Q S R H I
546 TCTTGACACCAITGTTGAGACTTTATCTAAGGATTCAGAGAAGATTATATGGGAGGAGATGTCATATCTGGAGAGATGGTGGAGAGACGCTTACCTAAATAACAA
182 L D T I V E T L S K D S R R K F I W E E M S Y L E R W W R D A S P N K Q
655 GAAGCTTTGACTAAATGGTTAAGGATGGGACGCTAGAGATTGTTGGAGGTGGCTGGGTTATGAATGATGAGGCTAATCATTATTTGCCATAATGGAACAGATAG
219 E A L T K L V K D G Q L E I V G G W V M N D E A N S H Y F A I I E Q I
764 CAGAGGGTAATATGTGGCTGAATGACACAATTTGGGTTATCTTCAAGAAATCTTGGGCTATAGATCCCTTTGGCTATTATCAACCAATGGCTTATCTTCCGCGGTAT
255 A E G M W L N D T I G V I P K N S W A I D P F G Y S S T M A Y L L R R M
873 GGGTTTTGAAACATGCTTATTCAAAGGACTCATTACGAGCTCAAGAAGACCTTGCCAGCATAAAGATCTTGAATATATTGGCGTCAGAGCTGGGATGCTATGGAA
291 G F E N M L I Q R T H Y E L K K D L A Q H K N L E Y I W R Q S W D A E
982 ACCACAGATATCTTTTCTATGATGCGGTTTTATTATACAGATATCCACACACTTGTGGACAGAGGCTGCAATTTGCTGTGCTGATTGATTTCGCTCGGATGCGGG
328 T T D I F V H M M P F Y S Y D I P H T C G P E P A I C C Q F D F A R M R
1091 GATTTAAGTATGAACCTTGTCCATGGGGAAGCAGCCAGTGGAGACCCACACTAGAAAATGTGCAAGAGAGGGCATTAAAGCTTCTGGATCAATACAGAAAAATCCAC
364 G F K Y E L C P W G K H P V E T T L E N V Q E R A L K L L D Q Y R K K S T
1200 TCTATATCGAATCTTCTTATACCTCTTGGAGATGATTTAGGTACATTCGATCGATGAAGCCGAGGCTCAGTTCCGTAACACTACAGATGTTGTTGATCAG
400 L Y R T N T L L I P L G D D F R Y I S I D E A E A Q F R N Y Q M L F D H
1309 ATCACTCTAATCTAGTCTAAACGAGAAGCAAGTTTGGTACTTGGAGGATTATTCAGAACAGTCCGAGAAGAAGCAGACAGATGAATATTCTCGCTCTGGTG
437 I N S N P S L N A E A K F G T L E D Y F R T V R E E A D R V N Y S R P G
1418 AGGTGGCTCTGGTCAGCTTGTGGTTTCCCTTCTCTGTCAGGTGACTTCTTACATATGCAGATAGGCAACAGACTATTGGAGTGGTTATTATGTTTCAAGACCTTT
473 E V G S G Q V V G F P S L S G D F T Y A D R Q Q D Y V S G I S Y V S R P F
1527 CTTCAAAGCTGTTGATCGTGTCTCGACATACCCCTTGGTGGAGCTGAGATCATGATGTCATTCTGCTAGGTTATTGCCATCGAATCAATGGAGAAATTTCCAACA
509 F K A V D R V L E H T L R G A E I M M S F L L G Y C H R I Q C E K F P T
1636 AGTTTACGTATAAGTTGACTGCTGCAAGAAGAAATCTGGCTCTTTCCAGCACCATGATGGGTAAGTGGAACTGCTAAGGATTATGTTGTACAAGATTACGCCACCC
546 S F T Y K L T A A R R N L A L F Q H H D G V T G T A K D Y V V Q D Y G T
1745 GGATGCATACCTTGAAGACCTTCAGATCTTATGTCTAAAGCAATCGAAGTTCTTCTGGGATCCGCAACGAGAAAGAAATCTGATCAATCCCATCTTTT
582 R M H T S L Q D L Q I F M S K A I E V L L G I R H E K E K S D Q S P S F F
1854 CGAGGCAGAGCAATGAGATCAAGATGATGCTCGGCCAGTTCAACAAGCAATGTGCTCCCGGGAAGAAATTCGCACACAGTTACTCTTCAATCCATCAGAACAG
618 E A E Q M R S K Y D A R P V H K P I A F I A A R E G N S H T V I L F N P S E Q
1963 ACAGAGAGAGGAGGTGGTGAAGGTTGTTGTAACCCGCTGAAATCTCGGTTTGGAGTCAAACTGGAGTGTGTCCCTAGCCAAATTTCTCTGAAGTGCAGCATGAGC
655 T R E E V T V V V N R A E I S V L D S N W T C V P S Q I S V S R P F
2072 ATACCAACTATTCAACCGGAGACATCGCCTTATCGGAAGCTTCCATCCAGCTCTTGGTCTGAGAACATATTTTCATTCGTAATGGGAATGTCGAGTGTGAGAAAGC
691 D T L T F G R H R L Y W K A S I P A L G L R T Y F I A N G N V E C E K A
2181 TACTCCGTCTAAACTCAAATACGCTTCTGAGTTTGACCCATTTCTGCTCTCTCCATATTCTGCTCCAACTGGACAACGACGTTACTGAGATCGAAATGAACAT
727 T P S K L K Y A S E F D P F P C P P P Y S C S K L D N D V T E I R N E H
2290 CAGACTCTTGTGTTGATGTGAAGAACGGATCACTGCGGAAGATAGTCCATAGAAACGGATCAGAGACTGTTGTGGGAGAAGAGATAGGTATGATCTAGTCCAGAGA
764 Q T L V F D V K N G S L R K I V H R N G S E T V V G E E I G M Y S S P E
2399 GTGGAGCTTACCTGTTCAAACAGATGGTGAAGCTCAGCCAATTTGTTCAACCTGATGGACATGATGTCACCTCTGAGGGTCTGCTGGTTCAAGAACTCTTCTCTACCC
800 S G A Y L F K P D G E A Q P I V Q P D G H V V T S E G L L V Q E V F S Y P
2508 TAAACCAAAATGGGAGAAATCACCCCTCTCTCAGAAAACCTCGTCTTACACTGGAGGTAAATACGCTTCAGGATCAAGTGGTCCGATAGAATATCATGTTGACCTCTT
836 K T K W E K S P L S Q K T R L Y G G N T L Q D Q V V E I E Y H V E L L
2617 GGTATGATTTTATGACCGGGAATGATTGTCGGGTACAGACTGATGTGACAAAGAAAGGTTCTTATTAGATCTCAATGGTTTCAAATGACGAGGAGAGAAA
873 G N D F D D R E L I V R Y K T D V D N K K V F Y S D L N G F Q M S R R E
726 CTTATGATAAGATCCCTCTTCAAGGAACTACTACCCAATGCCATCTCTCGGATTTATCCAAGGATCCAATGGTCAGAGATTCTCGGTGCACTCTCGTCAATCTCTCG
909 T T Y D K I P L Q G N Y Y P M P S L A F I Q G S N G Q R F S V H S R Q S L G
2835 TTTTGCAAGCCTCAAAGAGGTTGGTGGAGATTATGCTGGACAGACGGTTGGTCTGTGATGACGGACGGGTCTAGGGCAAGGTGTGATGGATAACCGCGCAATGACC
945 V A S L K E G W L E I M L D R L V R D D G R G L G Q G V M D N R A M T
2944 GTGGTATTTCACCTTCTTGGGAATCTAACATTTCTCAAGCAGACCTGCTTCAACACTAACCCGAGGAACCTTCTGCTTCTCTCACTCATAGGTGCTCACTTAA
982 V V F H L L A E S N I S Q A D P A S N T N P R N P S L L S H L I G A H L
3053 ACTACCCCAATAACACATTCTTGGCAAGAACCGCAGACATATCTGTGCTGTTCACAAATACGGTTCTTGGCTCTTTAGCCAAACCGTTACCATGTGACCTCCA
1018 N Y P I N T F I A K K P Q D I S V R T P Q Y G S F A P L A K P L P C D L H
3162 CATTTGAAATTTCAAGGTTCTCTGCTCCATCCAAATCTCTCAGCAATTTGGAAGAAGACAAGCCAAGTTGCTCTTATCTCTCAATAGACGAGCTTGGGATTGAGCTTAT
1054 I V N F K V P R P S K Y S Q L E E D K P R F A L I L N R A W D S A Y
3271 TGCCATAAAGGAAGACAGTAACTGCACAAGCATGGCTAATGAACCAAGTAACTTTCCGACATGTTCAAGATCTTGCAGCTTCAAGGTAACCACTCACTGA
1091 C H K G R Q V N C T S M A N E P V N F S D M F K D L A S K V K P T S L
3380 ATCTCTTGAAGAAGATATGGAGATTCTTGGTACGATGACCAAGAGCTACCTCGAGATAGTTACAGCCACGGGAAGGACGTGTCTCGATCTCTCCATGGAAATACG
1127 N L L Q E D M E I L G Y D D Q E L P R D S S Q P R E G R V S I S P M E I R
3489 AGCTTATAAGCTTGAAGTGGACCTCAACAAGTGA
1163 A Y K L E L R P H K
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FIG. 26

C. elegans Mannosidase II (NM_073594)

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1 ATGGCAAAACGCAATTTCTATATTATCTATGTTTGGGAGTCTTTCTCACCGTATCACTCTATTGTACAAATGGAATGAAACCGGAGCTGAAGCGCTCACCAAAACGACA
1 M G K R N F Y I I L C L G V F L T V S L Y L Y N G I E T G A E A L T K R Q
111 AGCAAAATGATTACGGCGGAAATCGAAATTTGGAGCATGTAGCAGAAGAAATGGAAGAACGATAGACCGCTTGAACACGAAGTTCAACGAGCAAAAGCTGAAAAAT
37 A N D L R R K I G N L E H V A E E R T I D R L E Q E V Q R A K A E K
221 CGGTAGATTTTGTATGAAGAAAAGAAAAACGGAAGAAAAAGAGTAGAAAAAGAGGAAAAAGAGTTGCACCGATTCCAGTTCCGAGGAAATCGTGGTGAATGGCTCAT
74 S V D F D E E K E K E V E K E E K E V A P V P V R G N R G E M A H
331 ATTCATCAAGTAAAGCAACATATCAAGCCAATCCATCGATGAAAGATGTTTGTGGATTAGAGAAAACGTCAGCATTGCTCATTGAGACCTGCAGATGCTCGATCTCTA
111 I H Q V K Q H I K P T P S M K D G G I R E N V S I A H S D L Q M L D L Y
441 TGACACCTGGAAGTTGAAATCCAGACGGAGGTGTATGGAAACAGGATGGAATTTGAATACGATGCAGAGAAAGTCAATCTCTTCCACGTTTGGAGCTTATTGTGA
147 D T W K F E N P D G G V W K Q G W K I E Y D A E K V K S L P R L E V I V
551 TACCTCATCTCATTTGATCCCGATGGATTGACTTTTGAAGAGTATTACAACAGACAACTCGCAATATTCTTGATGGAATGGCTAAACATTTGGCAGAAAAAGAC
184 I P H S H C D P G W I M T F E E Y Y N R Q T R N I L D G M A K H L A E K D
661 GAAATCGCGTTTATATATGCAAAATATCAATTTTGAAGTCTGCGGAGACAGGAGATGAAATTAAGAAAGTAAAGGATTTGGAAGCAGGAAAGTTGA
221 E M R F I Y A E I S F F E T W W R D Q A D E I K K K V K G Y L E A G K F E
771 AATTGTTACTGGCGGATGGTTATGACAGATGAAGCTAATGCACATTATCACTCAATGATCACTGAATTTGTCGAAGGACATGAATGGATTCAAAATCAITTTGGGAAAA
257 I V T G G W V M T D E A N A H Y H S M I T E L F E G H E W I Q N H L G K
881 GCGCATTCCCAATCTCATTTGCTCAATGATCCATCGGTTTATCACCATCAATGCCACATCTTCAACTTCTGCTAATTAACCAATGCTGTAATCAAGAGATTCAT
294 S A I P V K Q S H W S I D P F G L S P M P H L L T S A N I T A N I T A N I V I Q R V H
991 TATTCGGTGAACGTCAGCTTCTCTGAAAAAGATCTTGAATTTCTACTGGAGACAATTTTGGATCAACTGGACATCTGATCTTCTGTTACATAATATGCTCTTCTA
331 Y S V K R E L A L K K N L E F Y W R Q L F G S T G H P D L R S H I M P F Y
1101 CTCTTACGATATACCTCATACGTGTGGCCGAGAACCTGTGTTTCTGTCAATTCGATTTCCGTAGAAATGCCAGAAAGTGGAAAAATCATGTGATTTGGGAAATCCCTCCAC
367 S Y D I P H T G C G P E P S V C C Q F D F R R M P E G G K S C D W G I P
1211 AGAAAAATTAACGATGACAATGTGGCTCAGAGAGCTGAAATGATTTATGATCAATATAGAAAAAGTCAACTTTTCAAGAAATATGTAATTTTCAACCAATTTGAGAT
404 Q K I N D D N V A H R A E M I Y D Q Y R K K S Q L F K N N V I F Q P L G D
1321 GATTTCAGGTACGACATGATTTTGAATGGAATTCACAATATGAAACTATAAGAAATTTGTCGAATACATGAATTCGAATTCGAATTCGAATTCGAATTCGAATTCGA
441 D F R Y D I D F E W N S Q Y E N Y K K L F E Y M N S K S E W N V H A Q F G
1431 AACTCTTTCTGATTTTCAAGAAGCTTGATCTGCAATTTCTGGCTGTGGGAGCACTTCCAACTTTTCTGGAGATTCTTCACTTATGCGGACGAGATGATCAT
477 T L S D Y F K K L D T A I S A S G E A Q L P T F S G D F T Y A D R D H
1541 ATTTGAGTGGTACTTCACTTCCCGTCCATTTCTATAACAGCTTGATCGGGTTTCCCAACTATTTTAAGATCAGCTGAAATCGCCTTACCCTTGCATAATTTGAAGAA
514 Y W S G Y F T S R P F Y K Q L D R V L Q H Y L R S A E I A F T L A N I E
1651 GAAGGAATGGTTGAAGCGAAAAATTTTGAAGAGCTTGTGACTGCTCGACGAGCTCTTCACTTTTCCAACATCAGCATGGTGTAACTGGTACGGCAAAAGATCAGCTGT
551 E G M V E A K I F E K L V T A R R A L S L F Q H H D G V T G T A K D H V
1761 CTGGATTATGGTCAGAAATGATTGATGCTTTGAACGATGTGAGGATATCTTTTGGAGAGCTTGTGTTGATGCTGGGAATTTGATCAACGAATAAGATGCGATGG
587 L D Y G Q K M I D A L N A C E D I L S E A L V L L G I D S T N K M Q M
1871 ATGAGCATAGAGTTAATGAAACCTTACCCGAAAACTGTCTATAAAATTTGGGCAAAACGTCGATTTGTTCAATACCTTATCTAGAAATCGCAACGAGCAATTTGT
624 D E H R V N E N L L P E K R V Y K I G Q N V V L F N T L S R N R N E P I C
1981 ATTCAGTTGATTTCTTACGCTGGTGTGCAAGCTGATCCTCCAATTAAGAAACCAAGTTTCGCGGTTTATGATATGATGAAGAGAAGAAACGCTTGTGTCAA
661 I Q V D S L D A G V E A D P P I K K Q Q V S P V I A Y D E E K K T L V V K
2091 AAACGGAATATTGCAACTTTGCTTCATGTTTCACTTGGACCAATGGAGCTGTGCTGATTTGAGATTTGAAAAATACAACAATCCAAAGTTGAAATATCAACCAATA
697 N G I F E L C F M L S L G P M E S V S F R L V K N T T T S K V E I I T N
2201 ATGCGGCAGAAATCAAGAAACAGTTTAAATCTTCATCCACTTCTGGAGACTTACTGTGAAAAACGACAAAGTTGAAGCTGAATTTGATGGGAAAAATGGAATGAT
734 N A A E F K E T S F K S S S T S G D F T V K N D K V E A E F D G E N G M I
2311 AAAAGAGCTACCACTTGTGATGATAACCAATTTGATTTGAATTTCTCACTTATTCATTATGAGGACGCGGAAGTCAAAGAGAAAGTTCCGAAATGGAATGAAGCAA
771 K R A T S L V D D K P I D L N S H F I H Y G A R K S K R K F A N G N E D N
2421 CCCGCTGGCGCATACCTGTTCTTCCGATGGAGAAGCTAGAGAACTCAAAAAACAACTCAAGTGATTTGATATTTGGTAAAAAGGAGAAGTTGTTCAAAAAAGTTGTTGCAA
807 P A G A Y L F L P D G E A R E L K K Q S S D W I L V K G E V V Q K V F A
2531 CTCGCAACATGATCTGAAATATTGCAACGTCACACCTTTATCAAGGCTTCCATGGATTGATTTGGAATATGAAGTTGATGTACGTTTCAAGGAGAATTTGAGTTG
844 T P N N D L K I L Q T Y T L Y Q G L P W I D L D N E V D V R S K E N F E L
2641 GCATCGAGATTCAGTTCTTCACTAATAGTGTGATGATTTTCTCACTGATTCATGGAATGCAATGATAAAAGGAGACGACAACTAAATACCAACACAGGCCAA
881 A L R F S S S V N S G D E F F T D L N G M Q M I K R R R T K L P T Q A N
2751 TTTCTATCCATGCTGCTGGTGTTTTACATTGAAGACGATACCTACGATGATCAATTTCTCGGACAGGCTCTCGGAGTTAGCAGTCTCTGCTGGGACAAATTTGAAA
917 F Y P M S A G V Y I E D D T T R M S I H S A Q A L G V S S L S S G Q I E
2861 TAATGCTTGATCGACGACTTAGTTCAGATGACAAACAGAGGCTCTTCAAGAGGAGTTAGAGACAACAAACGAACAGTTCACATTTCCGTATTCTTATTGAGCCGATGCT
954 I M L D R R L S S D D N R G L Q Q G V R D N K R T V A H F R I V I E P M S
2971 TCATCGAGTGGTAAATAAGAAAGGAAGCAAGTGGATTCCATTACATGTTGGTCACTCGCTACGTTGGTCTCTTCAATTCCTCTTGTCAAAATGATTGGAGATGCAAC
991 S S S G N K K E E R V G F H S H V G H L A T W S L H Y P L V K M I G D A T
3081 ACCAAAAATCTATTTTGAAGAAATGTGAACAAGAGCTGAAGTGTGACCTGATCTAGTGACATTTAGAACACTGGCATCGCGGACAACTACGAGCAACCAAGCAAGAT
1027 P K S I S S K N V E O E L N C D L H L V T F R T L A S P T T Y E A N E R
3191 CTACGGCAGCTGAGAGAAAGCAGCGATGGTGTGATGATAGATTTTCCAGATGTAGATCCAGGCTTACCCTCCAGACACGTCATGCTTAGCTACTGATAGAAAT
1064 S T A A E K K A A M V M H R V V P D C R S R L T L P D T L S C L A T L E I
3301 GAGCCACTCAATTTGATCTCGACACTGAAGTCTCGGAAAAAACGTCACAAACCAATCTTTATGAAGGAAACAGGCTGAACAAATCCGACTCCAACCAACGATATTT
1101 E P L K L I S T L K S A K K T S L T N L Y E G N K A E Q F R L Q P N D I S
3411 CAGTATTTGATCATTTTAA
1137 S I L V S F
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FIG. 27

Ciona intestinalis mannosidase II (AK116684)

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1 ATGAAGCTCAACGCCAGTCTTATTCTTTGGTGGAAATCTGTTCTTCGGGAGTATCTGGTTTATGATAGGTCAACTTGACACTCCTAATTCGCCACAGAAAGTCAAA
110 TCTCGGAAGGCAGTGAAGATGACCAAGTTCGAACCTTCAACACAACTTAGTCTGGTGGAAAGAAATGTTAGAAAATCGTAAAAATATGCACAGGTGAAAGATAG
377 F S E G S E N D Q V R T L Q D K L S L V E K E L L E N R K I M H K V K D S
219 TCTACAGGATATGACACCCATGAAAAATGTTTCATGTCCTATGCAGCGCGGAGAAATAAGAAACCAACGTCAATAAACCTGTGTACCACTTATAATGCCCAAGCAATTT
73 L Q D M T P M K N V H V P M Q R G E I R N N V N K P V L P L I M P K Q F
328 GCGAATGACTCCCGAATGAGTGACCGTTCCTGTGCTCTCGTACTCCGGTGGCAAGTCCGATGTTAATGATTAACGTGTATGATCATCTTCCATTGTGATGATCCAG
110 A N D S R M S D T C P V L S Y S G G K S D V N M I N V Y D H L P F D D P
437 ATGGTGGAGTTTGGAAACAAGGTTGGGACATCCAGACATCGGATCAGGAATGGCTGGGAGAAAATGAAAGTGTTCATTGTCCCTCACTCACATAATGATCTCGGTTG
146 D G G V W K Q G W D I O T S D Q E W A G R K L K V F I V P H S H N D P G W
546 GTTAAAGACCGTGGAAAGATACCTTCAGCGATCAACACACATATTTCTCAATAATATTGTGGATGCTTTGAGTCAAGACCCCTGCAAGCAAGTTTATCTGGGCAGAGATG
182 L K T V E R Y F S D Q T H L N N I V D A L S Q D P A R K F I W A E M
655 TCGTATCTCTCAATGTGGTGGGACATGCCACACCTGATCGTAAGCAGAAAATGCAGACACTCGTGAAGAAATGGACAGCTTGAGATAGTTACGGGTGGTGGGTCATGA
219 S Y L S M W W D I A T P D R K Q K M Q T L V K N G Q L E I V T G G W V M
764 ATGATGAAGCAAACTCACTTACTTTGCTATGATTGATCAACTCATTGAAGGTATGGAATGGTTGAGGCGAACATTGAATGTTGTTCCAAAAGTGGGTGGCGGATTGA
255 N D E A N T H Y F A M I D Q L I E G M E W L R R T L N V V P K S G W A I D
873 TCCTTTGGTCACACCCCATGGCTTATATCTGAAACAGATGAAGTTCAAAAACATGCTGATACAAAGAGTCCATTATGCAGTGAAGAGATCTTGTCTCAGGAA
291 P F G H T P T M A Y I L K Q M K F K N M L I Q R V H Y A V K K Y L A Q E
982 AAGTCTCTGGAATTGAGATGGGACATGCCACACCTGATCGTAAGCAGAAAATGCAGACACTCGTGAAGAAATGGACAGCTTGAGATAGTTACGGGTGGTGGGTCATGA
328 K S L E F R W R Q M W D S A S S T D M M C H L M P F Y S Y D V P H T C G
1091 CAGACCCCAAGTTTGGTGGCAGTTTGTCTTACCGCGCGCAAGATAAATCTGCTTGGCAAGTTCCTCTGTCCTGTCATGACTGCAATGTAGAAAC
364 P D P K I C C Q F D F A R L P G G K I T C P W K V P P V A I T D S N V E T
1200 ACGAGCCGGAATACTACTTGACCAATATAGAAAAAGTCAAACTCTTCAAAAGTGACACCCCTGCTTATATATAGGAGATGATTTTCTGTTATTCGCTGAGCAGGAA
400 R A G I L L D O Y R K K S K L F K S D T L L I I L G D D F R Y S L S K E
1309 ACCAAGCATGAGTTGACAACTACGCTCGAATTATCTCGTATGTGAATTCCGACCCAGAGTTAAACGCAAACTTCAGTTTGGAAACATTATCCGAATATTTGATGCCA
437 T N D O F D N Y A R I I S Y V N S H P E L N A K L Q F G T L S E Y F D A
1418 TGAATCTGAAGTGGGGGAGAGGAAAACTCCAGCTTTAAGTGGTGATTTCTTCACTTATGCTGATAGAGAATCACTATTGGAGTGGTTACTACACTTACCGGCC
473 M K S E V G G E E K L P A L S G D F F T Y A D R E D H Y W S G Y Y T S R P
1527 TTACCAACAAATGCGAGGAGAGTCTCGAAGCCACCTTCGAGGAGCAGAAATGTTGTCGCTCTCATGGCCCAAAATCCAGTGGACAGGACTTTGTGAAACATTT
509 Y H K M Q E R V L E S H L R G A G A E M L F A L S W P K I Q W T G L G E T F
1636 TCACATGAACCTTACCCACTGCTGGTCCAAGCAGTCAAAATCTTGGTTTGGTTTCAACACCCAGAGTGAATACAGGCAAGGATCATGTTGTTGTTGTTGATTCAG
546 S H E L Y P L L V Q A R Q N L G L F O H H D G I T G T A K D H V V V D Y
1745 GGAATAAATCATGAAGAGTGTATGGATGCAAGAAGGTAATTTATACAGTGCACCAAGTTCTGTTGCAAGAAATGATCAGCTTTGATCCAAATACCATGTTACTTAA
582 G N K L M K S V M D A K K V I S Y S A Q V L L Q E M I T F D P N T M V L N
1854 CTATGATGAGGTGTATCAAGCTCAGAACCAACCACTCGCGCTGTGGTTGTTAAGCTACCAACGAAGATGAAGAAGCGCGGAAAGTCTGTTCTCTACAACTCTCTGGAT
618 Y D E V Y Q A Q N Q O P A P V V L L P T K N E E A R K V V L Y N S L D
1963 TACGACAGAACTGGTGTGCTGCGTCTAATTGTTACGTCAACCGAGCTGGTTGTGATGTGAGAAACAAACCTGCTTCCATCGCAACCACTGCTGATCTGGTCAGATT
655 Y D R T G V V R L I V T S P D V M S E N K N V V P S Q T S P I W S D
2072 CGACGGAGATCCGACACAGACAGTTTGAACGTGTTTCTTCAACTGTTCCTGCGATAGGACTGGCGGTGTACAAGATATGGGAAGACAACGACGTAGCAGACACCAC
691 S T E I R T D Q F E L V F L S T V P A I G L A V Y K I W E D N D V A D T T
2181 GCACCTCACTGTTAAGTTTATCAACCCGAGAGTTGGGTTTTGAAACGAACCCGAGTAAGTTTGTACTCGAGCTTGAGGATAGCGGGGAGTTTACCATCATGAATGAC
727 H S T V K F I N P R V G F S K R T R S K F V L D V E D S G E F T I M N D
2290 CAATTAGTTGCGCAITTTCTCGGACAAAACGGGATGCTGCAGTCAGTCAACCTGTGCGTGACACAGTTAAACCGCAGCTCGGAATTGAATTCGTGCTTATCTTCTC
764 Q L V A H F S G Q N G M L Q S V T T V R D N V K T Q L G I E F V A Y T S
2399 GTAATAAGAAAGACAAGAGCGGCTTACTTGTCTGCTGCTGGACGACACACCGCATGTAACAGAAATCCACCGACCGTTAGTAAGGATCATCAGGGGTCCAGT
800 R N K K D K S G A Y L F L P A G A C P H V T E S H R P L V R I I R G P V
2508 GATGTCAACCGGTGATGTTCTACTACCGAAGCTTCTGCATAAAGTTACCTATACACCGGTACTGGTGAGGACCGCAGTCTTAGGCGTCCACGCTCTCAACGACGTC
836 M S T V H V L L P N V L H K V T L Y T G T G A G T Q S L G V H V S N D V
2617 CACGTTAGAAGTGGTACGACAAACAAAGAACTCAGTATGAGGTTAAACAGCGAAGTTTATCGGGAAGCAATTCITACGGATTAAACGGTTTCAAATTCACCCCC
873 D V R T G Y D N K E L S M R L N S E V L S G S K F F T D L N G F Q I Q P
2726 GAACCACTGATTCTAACTGCCACTACAAGCAAACTTCAACCAATACCCACAATGGCGTTTATACAAGACGAAAAATCAAGATTAACTTTGTATGACCGGCCCAACCACT
909 R T T Y S K L P L Q A N F Y P I P T M A F I Q D E K S R L T L M T A Q P L
2835 GGGTGTGCTCTCACTGAAGTCAAGTCACTTCAAGTGGTTTGGATCGCGTTTAAATGCAGGACGACAAACAGGGGGTGGGTCAAGGTGTGAAGATAATTTACCAACT
945 G V A S L K S G Q L E V V L D R R L M Q D D N R G V G Q G V K D N L P T
2944 CCGAGAGTTTCTGATCATGCTGGAAGATGGACCGCTATTGCAGCGAAGAAAGCAAACTCGTCAGCGAAGCTCGCGTATCCATCTATGGCTGTATCAGTCACTCAT
982 P E S F V I M L E R W T A I A K E S K S A K L A Y P S M A V Y Q S S
3053 GGGAAATGTACACCAATACGTCCTAATGTGGTAAATGGGCGGTACATTTGAAAGAAATATACCGTCTGCTGCCACAGCTTTTACCATGCGACGTGCACGTGTTAAA
1018 W E L L H P I R P M S V N G P V H L K E D Y R S L P Q L P C D P V H V L N
3162 CTGCGAGCAATTCATTCTAAAGATGCAAGTGGCCCTACCGACCAATCGGCTCTGCTCTACACACAGTTGGGCGGCAATGCTCCTTGGACGCGGATAAGTATTTCAC
1054 L R A I H S K D A V A P T D Q S A L L L H T V G R E C S L D A D K Y F H
3271 CCAACGTGCTCATGCCAGCGGTCGAGAAATTTGGCTATCAGGATCTCGACGCTTTTACTAACTCTGGCATCGGGAAGACGCTCGCTGTCTTACAACACGACGCGTCTG
1091 P T C L M H G V E K L A I T I S T L F T N S G M R K T S L S L Q H D G S
3380 TGCTGGACAACCAAGCGGTATTACAGTTTCCCAATGGAGATACAAGCTTACAAAAATAGTACTGACGTAA
1127 L L D N Q G G I T V S P M E I Q A Y K I V L T
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FIG. 28

Drosophila mannosidase II (X77652)

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1 ATGTTGCGAATACGTCGGCGGTTGCTTGGTAATTTGCTCCGGCTGCCTGCTGTTTTCTCAGCCTGTACATAATCCTCAATTTTGGCGCGCGGAGCCACCAG
1091 A P E V C P M E T A A Y V S S H S S
110 TAAAGCCCAACTGAGAACATTGAGAACAGCTGCATGAGCTGGAAATGGTTGAGGAGCACGGGAGGAGATGCGGAATCTCAGGGCGGCTGTCGGCCAAACATC
371 I K P N Y E N I E N K L H E L E N G L Q E H G E E M R N L R A R L A K T S
219 CAATCGCGACGATCCAATAACACCTCCACTTAAAGTGGCTCGTTCCTCCGAGGCGAGGCGCAATGCCAAGATGTGGTCCCAAGACGTCGCCAATGTGGATGTACAGATGCTG
73 N R D D P I R P P L K V A R S P R P G Q C Q D V V Q D V P N V D V Q M L
328 GAGCTATACGATCGCATGTCTTCAAGGACATAGATGGAGGCGGTGCGAAACAGGGCTGGAACATTAAAGTACGATCCACTGAACTACACGCCCATCACAACTAAAG
110 E L Y D R M S F K D I D G G V W K G W N I K Y D P L K Y N A H H K L K
437 TCTTCGTTGTGCGGCACTCGCACACGATCCTGGATGGATTGAGACCTTTGAGGAATACTACGACGACACCAAGCACATCTGTCCAATGCACTACGGCATCTGCA
146 V F V V P H S H N D P G W I Q T F E E Y Y Q H D T K H I L S N A L R H L H
546 CGACCAATCCCGAGATGAAGTTCATCTGGCGGAAATCTCCTACTTTGCTCGGTTCTATCAGCATTTGGGAGAGAACAAAAGTCGAGATGAAGTCCATTGTAAAGAT
182 D N P E M K F I W A E I S Y F A R F Y H D L G E N K K L Q M K S I V K N
655 GGACAGTTGGAAATTTGACTGGAGGATGGTAATGCCGAGCAGGCGCAACTCCCACTGGCGAAACGTAAGTCTGCTGACGTCGACCGAAGGGCAACATGGTTGAAGCAAT
219 G Q L E F V T G G W V M P D E A N S H W R N V L L Q L T E G Q T W L K Q
764 TCATGAATGTCACACCCACTGCTTCTGGGCCATCGATCCCTTCGGACACAGTCCCACTGACATTTTGCAGAGAGTGGTTTCAAGAATATGCTTATCCAAAG
255 F M N V T P T A S W A I D P F G H S P T M P Y I L Q K S G F K N M L I Q R
873 GACCACTATTCTGTTAAGAAAGAACTGGCCCAACAGCGACAGCTTGAGTTCTGTCGGCCAGATCTGGGACAAACAAAGGGACACAGCTCTCTCACCACATGATG
291 T H S V K K E L A Q R Q L E F L W R Q I W D N K G D T A L F T H M M
982 CCGTCTACTCTGACGATCTCTCATACCTGTGGTCCAGATCCCAAGGTTTGTGTCGATTGATTTCAACGAATGGGCTCTCTCGGTTGAGTTGTCATGGAAGG
328 P F Y S Y D I P H T C G P D P K V C C Q F D F K R M G S F G L S C P W K
1091 TGCGCGCGGTACAATCAGTGATCAAAATGTGGCAGCAGCTCAGATCTGCTGGTTGATCAGTGAAGAAGAAGGCGAGCTGTATCGCAACAACTGCTGCTGATTCC
364 V P P R T I S D Q N V A A R S D G L L V D Q W K K K A E L Y R T N V L L I P
1200 GTTGGGTGACGACTTCCGCTTCAAGCAGAACACCGAGTGGGATGTGCGAGCGCTGAGCTACGAAAGGCTGTTGCAACACATCAACAGCGAGGCCCATCTCAATGTCCAG
400 L G D D F R F K Q N T E W D V Q R V N Y E R L F E H I N S Q A H F N V Q
1309 GCGCAGTTGCGCAGCACTGCAGGAATCTTTGATGCAGTGCACCGGCGAAAGGGCGGACCAAGCCGAGTTTCCACGCTAAGCGGTGACTTTTACATACGCGGATC
437 A Q G T L Q E Y F D A V H Q A E R A G Q A E F P T L S G D F F T Y A D
1418 GATCGGATAACTATTGGAGTGGCTACTACACATCCCGCCGTATCATAAAGCGCTGGACCGGCTCCTGATGCACTATGTACGTGACGAGAAATGCTTTCCGCTGGCA
473 R S D N Y W S G Y Y T S R P Y H K R M D R V L M H Y V R A E M L S A W H
1527 CTCCTGGGACGATGCGCCGATCGAGGAAGCTCTGGAGCAGGCGCGCAGGAGCTGTCATTGTTCCAGCACCACGCGATATACTGGCAGAGAAAACGACGTA
509 S W D G M A R I E E R L Q A R R E L S L F Q H H D G I T G T A K T H V
1636 GTCGTCGATACGAGCAACGATCGAGGAAGCTTTAAAGGCTGTCAAATGGTAATGCAACAGTGGTCTACCGATTGCTGACAAAGCCCTCATCTACAGTCCGGAG
546 V V D Y E Q R M Q E A L K A C Q M V M Q Q S V Y R L L T K P S I Y S P D
1745 TCAGTTTCTCGTACTTTACGCTCGACGACTCCCGCTGGCCAGGATCTGGTGGAGGACAGTGAACACCACATAATCTGGGCGAGGATATGCTCCCTCCAGCATGT
582 F S F S Y F T L D D S R W P G S G V E D S R T T I I L G E D I L P S K H V
1854 GGTGATGCACAAACCCCTGCCCATGGCGGAGCAGCTGGTGGACTTTTATGATCCAGTCCGTTTGAAGCGTTACCGACTTGGCAACAACTCCGGTGGAGGCTCAG
618 V M H N T L P H W R E Q L V D F Y V S S P F V S V T D L A N N P V E A O
1963 GTGTCGCGGTGGAGCTGCCACACGACACTCACAAGACTATCCACCCACAAGGCTCCACCAAGTACCGCATCTCTCAAGGCTCGGCTGCCGCCATCG
655 V S P V W S W H H D T L T K T I H P O G S T T K Y R I I F K A R V P P M
2072 GCTTGGCCACCTACGTTTAAACATCTCCGATTCCAAGCCAGAGCAGCACTCGTATGCATCGAATCTCTTGTCCGTAAAAACCCGACTTCGTTACCATTTGGGCAATA
691 G L A T Y V L T I S D S K P E H T S Y A S N L L L R K N P T S L P L G Q Y
2181 TCCGGAGGATGTGAAGTTTGGCGATCTCTGAGAGATCTATTGGCGGTTGGTAACGGACCCACTTGGCTTTTTCGGAGCAGGCTCTCTTAAGTCCATTACGTTACT
727 P E D V K F G D P R E I S L R V G N G P T L A F S E Q G L L K S I Q L T
2290 CAGGATAGCCACATGTACCGGTGCACTTCAAGTCTCTCAAGTATGGCGTTGATCGCATGGCGATAGATCCGGTGCCTATCTGTTCTCGCCCAATGGACAGCTTCCG
764 Q D S P H V P V H F K F L K Y G V R S H G D R S G A Y L F L P N G P A S
2399 CAGTCGAGCTTGGCCAGCCAGTGGTCTGCTGACTAAGGGCAAAGTGGAGTCTGCTCCGTGAGCGTGGGACTTCCGAGCGTGGTGACCCAGACGATATGCGCGGTGGTGC
800 P V E L G Q P V V L V T K G K L E S S V S V G L P S V V H Q T I M R G G A
2508 ACCTGAGATTCCGAATCTGGTGGATATAGGCTCACTGGACAAACAGGAGATCGTGATCCGCTTGGAGACGCATATCGACAGCGGCGATATCTTACACGGATCTCAAT
836 P E I R N L V D I G S L D N T E I V M R L E T H I D S G D I F Y T D L N
2617 GGATTGCAATTTATCAAGAGGCGCGGTTTGGACAAATACCTTTGACGGCCAACTATTATCCCATACCTTCTGGTATGTTTATTGAGGATGCCAATACCGCACTCACTC
873 G L Q F I K R R L D K L P L Q A I H P O G S T T K Y R I I F K A R V P P M
2726 TCCTCAGCGGTCAACCGCTGGGTGGATCTTCTTGGGCTCGGGCGAGCTAGAGATTGCAAGATCGTCCGCTGGCCAGCGATGAGAACCGCGCTGGGACAGGGTGT
909 L L T G Q P L G G S S L A S G E L E I M Q D R R L A S D D E R G L G Q G V
2835 TTTGGACAACAGCGGTGCTGCATATTTATCGGCTGGTCTGGAGAGGTTAACAAGTGTGTCGACCGTCAAAGCTTATCTGCGGCTATTTGACAAGTGGCCGA
945 L D N K P V L H I Y R L V L E K V N N C V R P S K L H P A G Y L T S A A
2944 CACAAAGCATCGCAGTCACTGCTGGATCCACTGGACAAGTTTATATTCCGTGAAATGAGTGGATCGGGGCACAGGGCAATTTGGTGGCGATCATCTTCCGCTCGTG
982 H K A S Q S L L D P L D K F I F A E N E W I G A Q G Q F G G D H P S A R
3053 AGGATCTCGATGTGCTGGTGTGACAGCTTAAACAGAGCTCGGCCAAAACCCAGCGAGTAGGCTACGTTCTGACCCGACCAATCTGATGCAATCGGCGACTCCAGA
1018 E D L D V S V M R R L T K S S A K T Q R V G Y V L H R T N L M Q C G T P E
3162 GGAGCATACACAGCTGGATGTGCTCCCACTACTGCCAATGTGGCGAGTGGAGCGCAGCAGCTGACTTCTGCAAGATTTGCAAGCACTTGGATGGCATGGTG
1054 E H T Q K L D V C H L P N V A R C E R T T L T F L Q N L E H L D G M V
3271 GCGCGGAAGTGTGCCCCATGGAACCGCGCTTATGTGAGCAGTCACTCAAGCTGA
1091 A P E V C P M E T A A Y V S S H S S
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FIG. 29

Human mannosidase II (U31520)

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1 ATGAAGTTAAGCCGCGAGTTCACCGTGTTCGGCAGTGGCACTCTCTGTGGTGATTCTCTGCTCTACCTGATGCTGGACGGGGTCACTTAGACTACCCGAGAAC
101 M K L S R Q F T V F G S A I F C V V I F S L Y L M L D R G H L D Y P R N
110 CGCGCCGCGAGGGCTCCTTCCTCAGGGCCAGCTCTCAATGTTGCAAGAAAAATAGACCAATTTGAGCGGTTTGCTAGCTGAGAATAATGAGATCATCTCAAAATTAG
117 P R R E G S F P Q G Q L S M L Q E K I D H L E R L L A E N N E I S N I R
219 AGACTCAGTCATCAATTTGAGTGAGTCTGTGGAGGATGGTCCGAAAAGTTCACAAAGCAATTTACGCCAAGGTGCTGGCTCAGATCTTCTGCCCTCACAATTATCCCTC
73 D S V I N L S E S V E D G P K S S Q S N F S Q G A G S H L L P S Q L S L
328 TCAGTTGACACTGCAGACTGTCTGTTGCTTCACAAAGTGGAAAGTCACAATTCAGATGTGCAGATGTTGGATGTTTACAGTCTAATTTCTTTGACAATCCAGATGGTG
110 S V D T A D C L F A S Q S G S H N S D V Q M L D V Y S L I S F D N P D G
437 GAGTTTGGGAAGCAAGGATTGACATTACTTATGAATCTAATGAATGGGACACTGAACCCCTTCAAGTCTTTGTGGTGGCTCATTCCCATAACGACCCAGGTTGGTGAA
146 G V W K Q G F D I T Y E S N E W D T E P L Q V F V V P H S H N D P G W L K
546 GACTTTCAATGACTACTTTAGAGACAAGACTCAGTATATTTTAATAACATGGTCTCAAGCTGAAAGAAGACTCAGGAGGAAGTTTATTTGGTCTGAGATCTCTTAC
182 T F N D Y F R D K T Q Y I F N N M V L K L K E D S R R K F I W S E I S Y
655 CTTTCAAAGTGGTGGATATTATAGATATTCAGAAGAAGGATGCTGTTAAAGTTTAAATAGAAAATGGTCAAGTTGAAATTTGACAGGTGGCTGGGTTATGCCTGATG
219 L S K W D I I D I Q K K D A V K S L I E N G Q L E I V T G G W V M P D
764 AAGCTACTCCACATTATTTGCCCTTAATGATCACTAATGAAGGACATCAGTGGCTGGAAAATAATATAGGAGTGAACCTCGGTCCGGCTGGGCTATTGATCCCTT
255 E A T P H Y F A L I D Q L I E G H Q W L E N N I G V K P R S G W A I D P F
873 TGGACACTCACCACAATGGCTTATCTTAAACCGTGTGGACTTTTTCACATGCTTATCCAGAGAGTTCATTATGCAGTTAAAAAACACTTTGCACTGCATAAAAA
291 G H S P T M A Y L L N R A G L S H M L I Q R V H Y A V K K H F A L H K T
982 TTGGAGTTTGTGGAGACAGAATGGGATCTGGGATCTGTACAGATATTTTATGCAAGATGATCCCTTACAGCTATGACATCCCTCAGCTTTGGGATGGGATG
328 L E F F W R Q N W D L G S V T D I L C H M M P F Y S Y D I P H T C G P D
1091 CTAATAATGCTGCCAGTTGATTTTAAACGCTTCTCGGAGGCGAGATTGGTGTGCTCGGAGGCTCCCGCCAGAAAACATACATCTCGGAAATGTCCAAAGCAGGCG
364 P K I C C Q F D K R L P G G R F G C P W G V P P E T I H P G N V Q S R A
1200 TCGGATGCTACTAGATCAGTACCGAAAGAGTCAAGGCTTTTTCGACCAAAAGTCTCTCGCTCCACTAGGAGATGATTTCGCTACTGTGAATACACGGAATGGGAT
400 R M L L D Q Y R K K S K L F R T K V L L A P L G D D F R Y C E Y T E W D
1309 TTACAGTTTAAAGATTATCAGCAGCTTTTGTATATATGAATTTCTCAGTCCAAGTTTAAAGTAAAGTACAGTTTGGAACTTTATCAGATTTTTTGATCGCTGGGATA
1418 AAGCAGATGAAACTCAGAGAGACAAGGCCAATCGATGTTCCCTGTTTAAAGTGGAGATTTTTCCTTATGCCGATCGAGATGATCATTACTGGATGGCTATTTTAC
473 K A D E T Q R D K G Q S M F P V L S G D F F T Y A D R D D H Y W S G Y F T
1527 ATCCAGACCTTTTACAAACGAATGGACAGAATCATGGAATCTCATTTAAGGGCTCTGAAATTTTACTATTTTCGCTGAGACAACTCACAATAACGAATAAAT
509 S R P F Y K R M D R I M E S H L R A A E I L Y Y F A L R Q A H K Y K I N
1636 AAATTTCTCTCATCATCTTTACACGGCACTGACAGAAGCCAGAGGAATTTGGGACTGTTTCAACATCATGATGCTATCACAGGAAGTCCAAAAGACTGGGTGGTG
546 K F L S S S L Y T A L T E A R R N L G L F Q H H D A I T G T A K D W V V
1745 TGGATTATGGTACCAGACTTTTTCATTGCTTAATGGTTTGGAGAAGATAATGGGAATTTGCAATTTCTTCTTATTGGGAAGGACAAACTCACAATCAGCTCTTACTC
582 V D Y G T R L F H S L V L E K I I G N S A F L L I G K D K L T Y D S Y S
1854 TCCTGATACCTTCTCGGAGATGGATTGAAACAAAATCACAAGATTTCTCGCCACAAAAAATAATAAAGGCTGAGTGGGAGCCAAAGGACTCTTGTGGTCTATAAT
618 P D T F L E M D L K Q K S Q D S L P Q K N I I R L S A E P R Y L V Y N
1963 CTTTGAACAAGACCGAATCTCGTGGTCTCAGTCTATGTAGTTCCTCCGACAGTGAAGTGTCTCTGCTTCAGGAAAACCTGTGGAGTTCAAGTCAGCGCAGTTT
655 P L E Q D R I S L V S V Y V S S P T V Q V F S A S G K P V E V Q V S A V
2072 GGGATACAGCAAAATACTATTTAGAAACAGCCTATGAGATCTCTTTTCAGACATATATCCGCCATTGGGACTGAAAGTGATAAGATTTTGGAATCAGCAAGTTCAAA
691 W D T A N T I S E T A Y E I S F R A H I P P L G L K V Y K I L E S A S S N
2181 TTCACATTTAGCTGATTATGTCTGTATAAGAATAAAGTAGAAGATAGCGGAATTTTACCATAAAGAAATATGATAAATCTGAAGAAGGTATAACACTAGAGAACTCC
727 S H L A D A Y V L Y K N K V E D S G I F T I K N M I N T E E G I T L E N S
2290 TTTGTTTTACTTCGGTTTGTATCAAACTGGACTATGAAGCAATGATGACTAAAGAAAGTGGTAAACACCATGAAGTAAATGTGAATTTTCATGGTATGGAACCAAA
764 F V L L R F D O T G L M K Q M M T K E D G K H H E V N V Q F S W Y G T T
2399 TTAAGAGAGACAAAAGTGGTGCCTACCTCTTCTTACCTGATGGTAAATGCCAAGCCTTATGTTTACACAACACCGCCCTTTGTGAGAGTGACACATGGAAGGATTTATTC
800 I K R D K S G A Y L F L P D G N A K P Y V Y T T P P F V R V T H G R I Y S
2508 GGAAGTGACTGCTTTTTGACCATGTTACTCATAGAGTCCGACTATACCAACAGGGAATAGAAAGGACAGTCTGTGGAAGTTTCCAATATTGTGCACATCCGAAAA
836 E V T C F F D H V T H R V R L Y H I Q G I E G Q S V E V S N I V D I R K
2617 GTATATAACCGTGAGATTGCAATGAAAATTTCTTCTGATATAAAAAGCCAAAATAGATTTTATACTGACCTAAATGGGTACCAGATTCAACCTAGAATGACACTGAGCA
873 V Y N R E I A M K I S S D I K S Q N R F Y T D L N G Y Q I Q P R M T L S
2726 AATTGCCCTCTCAAGCAATGTCTATCCCATGACCACAATGGCCTATATCCAGGATGCCAAACATCGTTTGACACTGCTCTGCTGCTCAGTCATTAGGGGTTTCAGATT
909 K L P L Q A N V Y P M T T M A Y I Q D A K H R L T L L S A Q S L G V S S L
2835 GAATAGTGGTCAGATTGAAGTTATCATGGATCGAAGACTCATGCAAGATGATAATCGTGGCCTTGAGCAAGGTATCCAGGATAACAGATTACAGCTAATCTATTTTGA
945 N S G Q I E V I M D R R L M Q D D N R G L E Q G I Q D N K I T A N L F R
2944 ATACTACTAGAAAAAGAGTGTCTTAATACGGAAGAAGAAAGAGTGGTCAAGTATCTCTCTCTTACCCACATAACTTCTCTCTCATGAATCAATCCAGTCA
982 I L L E K R S A V N T E E E K K S V S Y P S L L S H I T S L M N H P V
3053 TTCCAATGGCAAAATAGTTCTCTCCTCAGCTACCTTTGAGCTGCAAGGTGAATTTCTCCATTACAGTCACTTTTGGCTTGTGACATTCATCTGGTTAATTTGAGAACAAT
1018 I P M A N K F S S P T L E L Q G E F S P L Q S S L P C D I H L V N L R T I
3162 ACAGTCAAAGGTGGGCAATGGGCACTCCAATGAGGCAGCCTTGATCCTCCACAGAAAAGGGTTTGATTGTGCGTTCTCTAGCAAAAGGCAAGGCTGTTTGTCTACT
1054 Q S K V G N G H S N E A A L I L H R K G F D C R F S S K G T G L F C S T
3271 ACTCAGGGAAGATATTGGTACAGAACTTTTAAACAAGTTTATTTGCGAAAGTCTCACACCTTCATCACTATCCTTGATGCATTACCTCCCGGCACTCAGAAATATA
1091 T Q G K I L V Q K L L N K F I V E S L T P S S L S L M H S P P G T Q N I
3380 GTGAGATCAACTTGAGTCCAATGGAATCAGCACATTCGAATCCAGTTGAGGTGA
1127 S E I N L S P M E I S T F R I Q L R
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FIG. 30

Mouse mannosidase II (X61172)

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1 ATGAAGTTAAGTCGCCAGTTACCGGTGTTGGCAGCGCATCTTCTCGTCTGAATCTTCTCACTCTACCTGATGCTGGACAGGGGTCCTTGGACTACCCCTCGGGGCC
2 M K L S R Q F T V F G S A I F C V V I F S L Y L M L D R G H L D Y P R G P
111 GCGCCAGGAGGGCTCCTTCCGAGGGCCAGCTTTCAATATGCAAGAAAGATTGACCATTTGGAGCGTTTGGCTCGCTGAGAACACGAGATCATCTCAAAATACAGAG
37 R O E G S F P O G Q L S I L Q E K I D H L E R L L A E N N E I I S N I R
221 ACTCAGTCATCAACCTGAGCGAGTCTGTGGAGGACGGCCCGGGGGTACCAGGCAACGCCAGCAAGGCTCCATCCACCTCCACTCGCCACAGTTGGCCCTGCAGGCT
74 D S V I N L S E S V E D G P R G S P G N A S Q G S I H L H S P Q L A L Q A
331 GACCCAGAGACTGTTTGTGTTTCTTACAGAGTGGGAGTCAGCCCGGGATGTCAGATGTTGGATGTTTACGATCTGATTCCTTTTGATAATCCAGATGGTGGAGTTTG
111 D P R D C L F A S Q S G S Q P R D V Q M L D V Y Q L I P F D N P D G G V W
441 GAAGCAAGGATTTGACATTAAGTATGAAGCGGATGAGTGGGACCATGAGCCCTGCAAGTGTGTGGTGGCTCACTCCCAATAGACCCAGGTTGGTTGAAGACTTCA
147 K Q G F D I K Y E A D E W D H E P L Q V F V V P H S H N D P G W L K T F
551 ATGACTACTTTAGAGACAAGACTCAGTATATTTTAAATACATGGTCTAAAGCTGAAAGAAAGACTCAAGCAGGAAGTTTATGTGCTCTGAGATCTTTACCTTGCAAAA
184 N D Y F R D K T Q Y I F N N M V L K L K E D S S R K F M W S E I S Y L A K
661 TGTGGGATATTATAGATTTCCGAAGAAGGAGCTGTTAAAGTTTACTACAGAATGGTCAAGTGGAAATTTGACCGGTGGCTGGGTTATGCCTGATGAAGCCACTCC
221 W W D I I D I P K K E A V K S L L Q N G Q L E I V T G G W V M P D E A T P
771 ACATTATTTTCCCTTAATGACCACTAATTAAGGGCACCATGGCTGGAAAAAATCTAGGAGTGAAACCTCGATCGGGCTGGGCTATAGATCCCTTTGGCTATTAC
257 H Y F A L I D Q L I E G H Q W L E K N L G V K P R S G W A I D P F G H S
881 CCACAAATGGCTTATCTTAAAGCGTCTGGATTTTACACATGCTCTACAGAGATCTCATTATGCAATCAAAAAACACTTCTCTTGGCAAAAAAGCTGGAGTTTTC
294 P T M A Y L L K R A G F S H M L I Q R V H Y A I K K H F S L H K T L E F F
991 TGGAGACAGAATTGGGATCTGGATCTGCTACAGACATTTTGTCCCATATGATGCCCTTCTACAGCTACGACATCCCTCACACCTGTGGGCTGATCTAAATATGCTG
331 W R O N W D L G S A T D I L C H M M P F Y S Y D I P H T C G P D P K I C C
1101 CCAGTTGATTTTAAACGGCTTCTGGAGGCGAGATATGGTGTCCCTGGGGAGTTCCTCCAGAACCAATCTCCTGAAATGTCCAAAGCAGGGCTCAGATGCTATTGG
367 Q F D F K R L P G G R Y G C P V L S V P P E A I S P G N V Q S R A Q M L L
1211 ATCAGTACCGGAAAAAGTCAAACTTTTCCGCACTAAAGTTCTGCTGGCTCCACTGGGAGACGACTTTCGGTTCAAGTAATACACAGAGTGGGATCTGCAAGTGCAGGAAC
404 D Q Y R K K S K L F R T K V L L A P L G D D F R F S E Y T E W D L Q C R N
1321 TACGAGCAACTGTTTCAAGTACATGAAGTCCGAGCTCATCTGAAAGTGAAGATCCAGTTTGGAACTTGTGAGATATTTCGACGATTTGGAGAAAGCGGTGGCAGCGCA
441 Y E Q L F S Y M N S Q P H L K V K I Q F G T L S D Y F D A L E K A V A E
1431 GAAGAAGAGTACGAGCTGTGTTTCCCTGCCCTGAGTGGAGACTTCTTACGTAGCTGACAGAGACGACATTACTGGAGTGGGTACTTCAGCTCCAGACTTTCTACA
477 K K S S Q S V F P A L S G D F F T Y A D R D D H Y W S G Y F T S R P F Y
1541 AACGAATGGACAGATAATGAATCTCGTATAAGGGCTGCTGAAATCTTTTACAGTTTGGCTTGAACCAAGCTCAGAAATACAAGATAAAATTTCTTTCATCACT
514 K R M D R I M E S R I R A A E I L Y O L A L K Q A Q K Y K I N K F L S S P
1651 CATTACACAACTGACAGAAGCGAGAGAACTTAGGACTATTTACGATCATGATGCCATCACAGGAACCGGAAAGACTGGGTGGTTGGGACTATGGTACCAGACT
551 H Y T T L T E A R R N L G L F Q H H D A I T G T A K D W V V V D Y G T R L
1761 CTTTCACTTAAATCTTTGGAGAGATAATGGAGATTCTGCTTCTCTCTATTTAAAGCAAAAAAGCTGACAGTCAAGTCTTCCAAAGCCTTCTTAGAGA
587 F Q S L N S L E K I I G D S A F L L I L K D K K L Y Q S D P S K A F L E
1871 TGGATACGAAGCAAGTTTCAAGATTTCTTCCCAAAAAATTAATAACAATGAGCGCACAGGAGCAAGGTACTTGTGGTCTACAATCCCTTTGAACAAGAACGG
624 M D T K Q S S Q D S L P Q K I I I Q L S A Q E P R Y L V Y N P F E A C T
1981 CATTCACTGGTGTCCATCCGGTAACTCCGCCACAGGAAAGTGTCTGTGATTCCGGAAAAACCGGTGGAGGTTCAAGTCAAGTCAAGTTTCCAAAGCATGAGGACAAT
661 H S V S I R V N S A T G K V L S D S G K P V E V Q V S A V W N D M R T I
2091 TTCACAAGCAGCTATGAGGTTTCTTTTCTAGCTCATATACCACACTGGGACTGAAAGTGTTAAGATCTTAGAGTCAACAAGTCAAGCTCACACTTGGCTGATTATG
697 S Q A A Y E V S F L A H I P P L G L K V F K I L E S Q S S S S H L A D Y
2201 TCCTATATAAATGATGAGTACGAGAAATGGAATATTCCAGTGGAAGAACATGGTGGATGCTGGAGATGCCATAACAATAGAGAAATCCCTTCTGGGCAATTTGGGTTT
734 V L Y N N D G L A E N G I F H V K N M V D A G D A I T I E N P F L A I W F
2311 GACCGATCTGGGCTGATGGAGAAAGTGAGAAGAAAGACAGTACAGAGTGAAGTCAAGTCCAGTTCTGTGGTACGGAACCAACAAAAAGGACAGAGCGG
771 D R S G L M E K V R R K E D S R Q H E L K V Q F L W Y G T T N K R D K S G
2421 TGCTACCTCTCTCTGCTGACGGGCGAGGCCAGCCATATGTTTCCCTAAGACCGCCCTTGTGAGAGTGACACGTGGAAGGATCTACTCAGATGTGACCTGTTTCTCTG
807 A Y L F L P D G Q G Q P Y V S L R P P F V R V T R G R I Y S D V T C F L
2531 AACACGTTACTCACAAGTCCGCTGTACAACATTCAGGGAATAGAAGTCAAGTCCATGGAAGTTTCTAATATTGTAACATCAGGAATGTGCAATACCGTGAGATTGTA
844 E H V T H K V R L Y N I Q G I E G Q S M E V S N I V N I R N V H N R E I V
2641 ATGAGAATTTCACTAAAATAAACCAACAAATAGATATTATCTGACCTAAATGGATATCAGATTCAGCTTAGAAGGACCATGAGCAAAATGGCTCTTCAAGCCAAGT
881 M R I S S K I N N Q N R Y T D L N G Y Q I Q P R R T M S K L P L Q A N V
2751 TTACCCGATGTGCAATGGCGTATATCCAGGATGCTGAGCACCGGCTCAGCTGCTCTGCTCAGTCTCTAGGTGCTTCCAGATGGCTTCTGGTCAGATTGAAGTCT
917 Y P M C T M A Y I O D A E H R L T L L S A Q S L G A S S M A S G Q I E V
2861 TCATGGATCGAAGGCTCATGAGGATGATAACCGTGGCTTGGGCAAGGCGTCCATGACAATAAGATTACAGCTAATTTGTTTGAATCTCTCGAGAAGAGAACGCGT
954 F M D R R L M Q D D N R G L G Q G V H D N K I T A N L F R I L L E K R S A
2971 GTGAACATGGAAGAAGAAAGAGAGCCCTGTGAGTACCCTTCCCTCTCAGCCATGACTTCTGCTTCTCTCAACCATCCCTTTTCCCATGGTACTAAGTGGCCA
991 V N M E E E K K S P V S Y P S L L S H M T S S F L N H P F L P M V L S G Q
3081 GCTCCCTCCCTGCTTGTAGCTGCTGAGTGAATTTCTCTGCTGCTGCTCTCTACCTTGTGATATCCATCTGGTCAACCTCGGACAAATACAATCAAGATGGGCA
1027 L P S P A F E L L S E F P L L Q S S L L P C D I H L V N L R I Q S K M G
3191 AAGGCTATTCCGATGAGGAGCCTTGTATCTTCCACAGGAAGGCTTGTGATGCGAGTTTCTCAGCAGAGGACATCGGGCTACCTGTTCCACTACTCAGGGAAGATGTCA
1064 K G Y S D E A A L I L H R K G F D C Q F S S R G I G L P C S T T Q G K M S
3301 GTTCTGAACTTTTCAACAAGTTTGTCTGTGAGAGTCTGCTCCCTTCTCTGCTCTGATGCACTCCCTTCCAGATGCCAGAACATGAGTGAAGTCAAGCTGAGCCC
1101 V L K L F N K F A V E S L V P S S L S L M H S P P D A Q N M S E V S L S P
3411 CATGGAGTACGACGCTTCCGTATCCGCTTGGCTTGGAGCTGA
1137 M E I S T F R I R L R W T
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Rat mannosidase II (XM 218816)

[illegible]

Human mannosidase IIx (D55649)

1 ATGAAGCTGAAAAAGCAGGTGACAGTGTGTGGGGCTGCCATCTTCTGTGTGGCAGTCTTCTCGCTCTACCTCATGCTGGACCGAGTGCAACACGATCCCACCCGACAC
3 M K L K K K Q V T V C G A A I F C V A V F S L Y L M L D R V Q H D P T R H
110 AGAATTGTGGGAAGCTTCCCGGAGCAAAATTCTGTGTCGAGAACCGAATGAGCAGCTGGAGCAGCTTTTGGAGGAGAACCATGAGATATCAGCATATCAAGGA
37 Q N G N G F P R S Q I S V L O N R I E Q L E Q L L E E N H E I I S H I K D
219 CTCCTGCTGGAGCTGACAGCAACGACAGAGGGGCCGCCGCTACTACACGCTCAATGGCTCTGGGTGGTGCCACCGGAGCCCGGCCGAGCTTCTTC
73 S V L E L T A N A E G P P A M L P Y Y T V N G S V V P P E P R P S F F
328 TCACATCTCCCCGAGGAGTCCGAGTTTGCTTTGGGGGGCCGGGGTCAGAAAGCCAGAGCTGCAGATGCTCACTGCTCGGAGGAGCTGCCGTTTGACAACTGGGATGGTG
110 S I S P Q D C Q F A L L G R G Q K P E L Q M L T V S E E L P F D N V D G
437 GTGTGTGGAGGACGGCTTCGACATCTCTACGACCGCAGCAGCTGGGATGTGGAAGACTCGAGGTGTTTGGTGGCCCCACTTCACAATGACCCAGGCTGGATCAA
146 G V W R Q G F D I S Y D P H D W D A E D L O V F V P H S H N D P G W I K
546 GACCTTTGACAAGTACATACAGAGCAGACCCAAACACATCCTCAATAGCATGGTGTCTAAGCTGCGAGGAGGACCCCCGGCGGGCTTCTCTGGGCAGAGGCTCTCTT
182 T F D K Y Y T E Q T Q H I L N S M V S K L G D E D P R R R F L W A E V S F
655 TTCGCAAGTGGTGGGACAACTCAATTGCTCAAAAGAGAGCGCGCATCGGAAGCTGGTGGGAAAGCGGACCTGGAGATTGCGACAGGAGGCTGGGTGATGCCAGATG
219 F A K W W D N I N V Q K R A V R L L V L V G N G Q L E I A T G G W V M P D
764 AGGCCAATTCCTCACTATTGCTATTGATGACCCGCTCATCAAGGACCAAGCTGGCTGGAGAGAACTCTTGGTGCAACCCCGCTCTGGCTGGGACGTGGACCCCTT
255 E A N S H Y F A L I D Q L I E G H Q W L E R N L G A T P R S G W A V D P F
873 TGGATACAGCTCCACCATGCTTACCTGCGCCGCTGCCAACCTCACCAGCATGCTGATTGAGAGAGTGCACTATGCCATCAAGAAGCACTTGTCTGCCACCCACG
291 G Y S S T M P Y L L R R L N A N L T S M L I Q R V H Y A I K K H F A A T H S
982 CTAGAGTTTCATGTGGAGGACAGATGGGACTCGGACTCGGACCGACAGACATCTTCTGTACATGATGCCCTTCTACAGCTATGACGTCGCCCATCTGCTGGCCGAGATC
328 L E F M R T T W D S D S T D I F C H M P F Y S Y D V P H T C G P D
1091 CCAAGATCTGCTGCCAATTGATTTCAAAGCCCTGCTGCTGGGGCCTCAACTGCTTGGAAAGTGCACCCCGGGCCATCACAGAGGCCAACGTGGCAGAGAGGGC
364 P K I C C Q F D F K R L P G G R I N C P W K V P P R A I T E A N V A E R A
1200 AGCCCTGCTTCTGGACCAATACCGGAAGAAGTCCCGAGTGTTCCGAAGCAAGCTCTCTGCTGCTCTTGGAGATGACTTCGATATCAAGAAGCCAGGAGTGGGAT
400 A L L D D Q Y R K S Q L F R S N V L L V L G D D F R Y D K P Q E W D
1309 GCCCAGTTTCTCAACTACCAAGGCTTTGACTTCTTCAAGCAGGCTCAACTCCTATGTGACGGCCAGTTTGGCATCTTCTGCACTATTTTGATGCCCTGTACA
437 A Q F F N Y Q R L L F D F F N S R P N L H V Q A Q F G T L S D Y F D A L Y
1418 ACAGGACAGGGGTGGAGCCAGGGGCCGGCTCCAGGGTTTCTGCTGCTGAGCGGGGATTCTTCTCTCTATGCGGACCGGGAGGATCATTAAGTGGACAGGCTATTACAC
473 K R T G V E P G A R P P G F P V L S G D F F S Y A D R E D H Y W T G Y Y T
1527 TTCCCGGCCCTTCTACAAGAGCTTAGACCGAGTCTGGAAGCCCACTCGGGGGGACAGAGTTCTGTACAGCCTGGCTCGACCTCAGCTCGCCGCTCTGGTCTGGCT
509 S R P F Y K S L D R V L E A H L R G A E V L S L A A H A R R S G L A
1636 GGGCGCTACCACTGCTGATTTCACCTCTCTGACGGAAGCTCGGGCCACATTTGGGCTCTTCCAGCATCAGATGCCATCTGGCACGGCCAGGAGGCTGTGGTGG
546 G R Y P L S D F T L L T E A R N T L G L F Q H D A I T G T A K E A V V
1745 TGGACTATGGSGTCAGGCTTCTGCGCTCCCTTGTCAACCTGAAGCAGGTTCATCATTATGACGCCCACTATCTGGTGCTGGGGGACAGGAGACCTACCACTTTGACCC
582 V D Y G V R L L R S L V N L K Q V I I H A A H Y L V L G D K E T Y H F D P
1854 TGAGGCGGCTTCTCCAAGTGGATGACATCGTTAAGTCACAGCGCCTCCAGAGGCGACGGTATCAGCTGGATTCTCGGCCAGGTTTGGTGTCTATTCAAC
618 E A P F L Q V D O T R L T S H D A L P E R T V I Q L D S S P R F V V L F N
1963 CCACTGGAACAGGAGCATTACAGATGGTGCTCTGCTGCTCACTCCCGCGTCCGTGTCTTTCGGAGAGGGTCAGCCCTGGCCGTGCAGATCAGCGCACCT
655 P L E Q E R F S M V S L L V N S P R V R V L S E E G Q P L A V Q I S A H
2072 GGAGCTTCCGACCGAGGCGGTCCCTGACGCTCACCAGGTGCTGTGCTCTCGCGCTGCCAGCCTTGGGCTGGGCTGCTGCACTACAGCTGGGCTGGATGGGCA
691 W S S A T E A V D P V Q V S V P V R L P A L G L G V L Q L O L G L D H
2181 CCGCAGCTGCGCTCCTCTGTGCGCATCTACCTGCACGCGCGGAGCTGTCCGTGACAGGACCAAGACGTTTCTCTCTCGGTGATGACTCTGGCACAGGACCTTC
727 R T L P S S V R I Y L H G R Q L S V S R H E A F P L R V I D S G T S D F
2290 GCCCTCAGCAACCGCTACATGCAAGTGTGGTCTCAGGCTCTACTGGGCTCTCAAGAGCATCCGAAGGGTGGATGAGGAGCAGCAGCAGGTTGGACATGCAGGTCT
764 A L S N R Y M Q V W F S G L T G L L K S I R R V D E E H E Q V Q D M Q T
2399 TTGTCTATGGCACCCTGACGTCCAAAGACAAGAGTGAGGCTACCTCTCTCTGCGGATGGCGGAGGCTAGCCCTACGTECCCAAGGAGGCCCGGCTGCTGCGTCACT
800 L V Y G T R T S K D K S G A Y L F L P D G E A S P T S P R S P P C C V S L
2508 GAAGGCCCTTCTCTCAGAGTGGTGTGGCTACTATGACCAATCACCAGCGGTCGGCTTACAACTCTGCCAGGGGTGGAGGGCTGTCTTGGACATATCATCCC
836 K A L S Q R W L R T M S T F T R R S G F T I C G Q W R G C L W T Y H P
2617 TGGTGGACATCCGGGACTAGCTCAACAGAGAGTGGGCTGCACATCCATACAGACATCGACAGCCAGGGTCAGGCCCCAGCGGATCTGAAGAAGCTCCCCCTCAGG
873 W W T S G T T S T R S W P C T S I O T S T A R V Q P R Y R L K K L P L Q
2726 CCAACTCTACCCATGCCAGTCATGGCTATATCCAGGACGACAGAGCGGCTCAGCTGCACATCGCCAGGCGCTGGGTGTCTCTAGCTCAAGAATGGCCAGCT
909 A N F Y P M P V M A I Q D A Q K R L L H T A Q A Q L G V S S L K D G O L
2835 GGAGGTGATCTTGACAGCGCGGCTGATGAGGATGACAACCGGGGCTAGGCCAAGGGCTCAAGGACAACAGAGAACCTGCAACCGTTTCCGCTCTCTGCTAGACGG
945 E V I L D R R L M Q D D N R G L G Q G L K D N K R T C N R F R L L R
2944 CGAAGCGTGGGCACTGAGGTCCAAGATAGCCACTTACCAGCTACCCATCCCTCCTCAGCCACCTGACCTCCATGTACCTGAACGCCCGGGCGCTCGCTGCTGCTGAG
982 R T V G S E V Q D D S H S T S Y P S L S L S H L T S M Y L N A P A L A L P V
3053 CCAGGATGAGCTCCAGGCGCTGGTCTGCGCTATTTCATCTTGGCTTCTCAGCTGCTGACTTCACTGCTCAACTAGCTACGCTCAGGCTCAGGCTGAGGAGGA
1018 A R M Q L P G P G L R S F L C T S H P L P C D F H L L N L R T L Q A E E D
3162 CACCTTACCTCTCGGCGGAGCCGCACTATCTTACCCGCAAGGGTTTGAAGTGGGCTGGAGGCAAGAACTTGGGCTTCAACTGCACCAAGCAAGCAAGGTA
1054 T L P S A G E A T A L I L H R K G F D C G L E A K N L G F N C T T S Q G K V
3271 GCCCTGGGCAACCTTTCCATGGCCTGGATGGGATTCTCTCAGCCAACTCTTGACGTTACTGTACCTCTGGGCTCCCCGCTCCAGAGCATGACGTTCTATTGG
1091 A L G S L F H G L D V V L F L Q P T S L T L L Y P L A S P S N S T D V Y L
3380 AGCCCATGGAGATTGCTACCTTTCGCTCCGCTCGGTTGGGTAG
1127 E P M E I A T F R L R L G

FIG. 33

Insect cell mannosidase III (AF005034)

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1 ATGAGGACTCGTGTCTTCTGTTGCCGGCGTCTCCACCCGGATCCTGCTGCTGCTATTGCTCTGCTTTGGGGTCTACTGCTATTCTACAATGCATCTCTCA
111 M R T R V L R C R P F S T R I L L L L L F V L A F G V Y C Y F Y N A S P Q
371 GAACATATAACAAACCAAGATCAGTTACCCAGCCGATGGAGCACTTCAATCTCCCTCACTCACACCGTCAAGAGCCGAGACGCAACTCCGGATCAATGCCCTG
371 N Y N K P R I S Y P A S M E H F K S S L T H T V K S R D E P T P D Q C P
221 CATTGAAGGAAGGCGAAGCGGACATCGACACCGTGGCGATATACCCAACTTTTGATTTTCAGCCGAGCTGGTTCGTAACAAAGGAATTTGGGACAAGTCTTCGAGGAT
741 A L K E S E A D I D T V A I Y P T F D F Q P S W L R T K E F W D K S F E D
331 CGGTATGAAAGAATTCTAACGACACTACCGGCTAGACTGAAGTAATCGTGGTCTCTCACTCACACAACGACCGGGATGGCTGAAGACGTTTGAACAGTACTTCGA
111 R Y E R I H N D T T R P R L K V I V P H S H N D P G W L K T F E Q Y F E
441 GTGGAAGACCAAGAACATTATCAACACATAGTGAACAACTGCACCACTACCCCAACATGACCTTCATTGGACCGAGATATGCTTTCTGAATGCCGTGGGAAAGGT
1471 W K T K N I I N N I V N K L H Q Y P N M T F I W T E I S F L N A W W E R
551 CGCACCTGTCAACAAAAGGCAATTGAAAAAATTATCAAGAAGGTCTGCTGAGATCAGACGGGCGGCTGGGTGATCGCGGACGAAGCCTGCACGCATATCTATCGG
1841 S H P V K Q K A L K K L I K E G R L E I T T G G W V M P D E A C T H I Y A
661 CTAATTGACCAAGTTTATGAAGGACATCACTGGGTGAAACATAATCTCGGCGTCACTCCGAGACAGGATGGTCTATTGACCCCTTCGGCCACGGGGCACTGTGCCTTA
2211 L I D Q F I E G H H W V K T N L G V I P K T G W S I D P F G H G A T V P Y
771 CCGTACAGACGAGCGGCTTCAGGGAACATTATACAGAGAATCCATTATGCTGGAAACAGTGGCTGGCGAGGACAGATTGAGGAGTTTACTGCGTGGCGAGTT
2571 L L D Q S G L E G T I I Q R I H Y A W K Q W L A E R Q I E E F Y W L A S
881 GGGCTACTACGAAGCGCTCCATGATAGTGCACAACTCAGCCGTTTGAATTTATTTCAATAAAAAGCACGTTGGCCCGCACCTTCAATTTGCTCAGTTTCGACTCAGG
2941 W A T T K P S M I V H N Q P F D I Y S I K S T C G P H P S I C L S F D F R
991 AAGATTCCCGCGCAATTTCTGAATACACAGCTAAGCAGAGACATCCGGAACACACTTGCACAGCAAGGCAAGACTTTGATAGAGGAGTACGACCTGATCCGGTC
3311 K I P G E Y S E Y T A K H E D I T E H N L H S K A K T L I E E Y D R I G S
1101 CCGTACTCCACAACTGGTGTGCTGGTGGCGTCCGAGACGACTTCAGATACGACTACAGCGTTCGAGTTGATGCCAATACGCTCAATTTATAGAAATGTTTAACTACA
3671 L T P H N V V L V L P L G D F R Y E Y S V E F D A Q Y V N Y M K M F N Y
1211 TCAATGCTCACAAGGAATCTTCAACGCTGACGTACAGTTCCGAACTCTCTCGATTACTTTAACGCCATGAAAGAAAGACATCAAAATATACCCAGCTTAAAGGGAGAT
4041 I N A H K E I F N A D V Q F G T P L D Y F N A M K E R H Q N I P S L K G D
1321 TTCTCTGTTTACTCCGATATTTTCAGCGAAGGTAACCCAGCGTACTGGTCAAGTTACTACTACTAGACCTACCAAAAAATCCTCGCCCGTCAAGTTCGAAACCAACT
4411 F F V Y S D I F S E G K P A Y W S G Y Y T T R P Y Q K I L A R Q F E H Q L
1431 GCGATCGGAGAGATTTTATCCCTTGTATCGAATCATACAGAGATGGGTGCCCAAGGAGAGTTCCGAGCTTCTGAGAAAAAGTTAGAAAAATCTTACGAGCAGC
4771 R S A E I L F T L V S N Y I R Q M G R Q G E F G A S E K K L E K S Y E Q
1541 TTATCTATGCTCGACGGAATCTGGTCTGTTTCAACATCAGGATCGGATTACTGGAACTCAAAAGTCCAGTGTGATGCAAGATTACGGAACCAAACTGTTTCAACAGCTG
5141 L I Y A R R N L G L F Q H H D A I T G T S K S S V M Q D Y G T K L F T S L
1651 TATCACTGCATCCGCTGCGAGGCGCGCTCACCACCATCATGTTGCTGACCACTGCTTGCCTGACGAGTGTGCTGACGAGCATTATACAAAGCGAGGTTGAGTGGGAACTTACGG
5511 Y H C I R L Q E A A L T T I M L P D Q S L H S Q S I I Q S E V E W E T Y G
1761 AAAACGCCCAAGAGCTGCAAGTGTCTTTCATTGACAAGAAAGTATTAATCTTTCGCTGGCTGAGACTCGAAGTGAAGTGTGACGCTTAGATCCAAAGCT
5871 K P P L L Q V S F I D K K V I L F N P L A E T R T E V T V R S N T
1871 CCAACATCCGGGTGATACGATACACAAAGAGGAGCAGCTTGTATCAGATAATGCCAGCATCAACATCCAAGACAACGGCAAGAGTATCGTAAGCGACACCAAGCTT
6241 S N I R V Y D T H K R K H V L Y Q I M P S I T I Q D N G K S I V S D T T F
1981 GACATAATGTTTCGTGGCCACCATCCCGCCCTCACCCTCATCTCGTACAAGTGCAGGAGCACACCAACTTCCCACTGCGTCAATTTCTGCAACAACTGCGGAACA
6611 D I M F V A T I P L T S I S Y K L Q E H T N T S H C V I F C N N C E Q
2091 ATACCAGAAATCCAATGTGTTCCAAATTAAGAAATGATGCTGCTGACATACAATAGAAATGCAAGTGTCTTCTGTTAATAGGAACACCGGCTTCTGAGAC
6971 Y Q K S N V F Q I K K M M P G D I Q L E N A V L K L L V N R N T G F L R
2201 AAGTCTATAGAAAGGACATCCGGAAGAGAACTGCTGTTGACGTACAATTCCGCGCATACAAAGTGCCCAAGACATTCTGGTGTCTTACCTCTTCATGCTCATTACGAC
7341 Q V Y R K D I R K R T V V D V Q F G A Y Q S A Q R H S G A Y L F M P H Y D
2311 TCACCTGAGAAGAATGTTCTGCATCCCTACACTAATCAGAACACATGCAAGATGATAACATAATCATAGTGTCCGGACCTATTTCTACGGAATCAGGACCATGTACTT
7711 S P E K N V L H P Y T N Q N N M Q D D N I I I V S G P I S T E I T T M Y L
2421 GCCCTTCTTGGTGCACACTATTAGGATATACAACTGCGCGGACCCGGTACTGCTGCGTGTCTATTCTATTAGAGACCGATGATAGATTTCGAGCGCCACCTAAGAACAGAG
8071 P F L V H T I R I Y N V P D P V L S R A I L L E T D V D F E A P P K N R
2531 AGACTGAGTTATTATGACATTACAGCTGATATACAAACCGGTGACATTCGCGAATTTTACACCGATCAGAACGGATTCCAGTACCAAAAGAGGGTCAAAGTGAATAAA
8441 E T E L F M R L Q T D I Q N G D I P E F Y T D Q N G F Q Y K R V K V N K
2641 CTAGGAATAGAAGTAATTAACCCGATCACTACCATGGCGTGCCTGCAAGACGAGGAGACCCGGTCACTCTGCTGACGAACCCGCTCAAGGCGCTGCTGCATACGA
8811 L G I E A N Y P I T T M A C L Q D E T R L T L L T N H A Q G A A Y E
2751 ACCAGGACGCTTAGAAGTCATGCTCGATCCTCGAATCTTTATGATGACTTCAGAGGAATCGGTGAAGGAGTAGTCGATAACAAACCGACGACTTCCGAACTCGATT
9171 P G R L E V M L D R R T L Y D D F R G I G E G V V D N K P T T F Q N W I
2861 TAATTGAATCCATGCCAGGCGTACGCGAGCAAGAGAGACACTAGTGAACAGGTTTCAAATTTGTTAATGAACGTCGTTTTGGCCCGGCGCAAGAGGAAGCCCTTAC
9541 L I E S M P G V T R A K R D T S E P G F K F V N E R R F G P G Q K E S P Y
2971 CAAGTACCGTCGACACTCGGACTACCTGAGCAGGATTTCAATTAACCGGTGAACGTGTACCTGGTGACACTAGCGAGGTTGGCGAGATCGAGGTGAAGCCGTACCA
9911 Q V P S O T A D Y L S R M F N Y P V N V Y L V D T S E V G E I E V K P Y Q
3081 GTCGTTCTGTCAGAGCTTCCCGCCCGGCTACCTGGTCAACCTCGCCACCATCACCAGCAGGTCGCTCGAATCTTCCCGACCAACGAAGCTACATGGTACTGCACC
10271 S F L Q S F P P G I H L V T L R T I T D D V L E L F P S N S Y M V L H
3191 GACCAGGATACAGCTCGCGTGTGCGAGAGAAGCCATCGCCAAAGTCTCCAAAGTTTTCGTCCTCAAAACAGGTTCAATGGTCTGAACATTGAGAATCACTGCACTGAGC
10641 P G Y S C A V G E K P V A K S P K F S S K T R F N G L N I Q N I T A V S
3301 CTGACCGGCTGAAGTCACTCCGACCTCTCAGGCTGAGTGACATCCACCTGAACGCTATGGAGTAAAACTTACAAGATCAGGTTTAA
11011 L T G L K S L R P L T G L S D I H L N A M E V K T Y K I R F
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FIG. 34

Human lysosomal mannosidase II (NM_000528)

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1 ATGGGCTACGCGGGGCTTCGGGGGTCTGCGCTCGGGGTGCTGGACTCAGCAGGCCCCCTGGACCATGTCCCGCGCCCTGCGGCCACCGCTCCCGCTCTCTGCTTTT
101 MGYARASGVCAARGCLDSAGPWTMSRALRPLPLPLCF
110 TCCTTTTGTGCTGGCGGCTGCGGTGCTCGGGCGGGGATACGAGACATGCCCCACAGTCGAGCCGAACATGCTGAACGTGCACCTGCTGCTCACACATGATGA
37 FLLLLLAAGARAGGYETCTPTVQPNMLNLNHLPLPHTHD
219 CGTGGGCTGGCTCAAAACCGTGGACAGTACTTTATGGAATCAAGAATGACATCCAGCAGCGCGGTGTGACATACATCTGACCTCGGTCTCTGCTTGTGGCA
73 V G W L K T V D Q Y F Y G I K N D I Q H A G V O Y I L D S V I S A L L A
328 CATCCACCCGCTCGCTTCATTACGTGGAGATGGCTTCTTCTCCGTTGGTGGCAGCAGACAAATGCCACACAGGAAGTCGTGCGAGACCTTGTGCGCCAGGGGC
110 D P T R R F I Y V E I A F F S R W W H Q Q T N A T Q E V V R D L V R Q G
437 GCCTGGAGTTCGCAATGGTGGGTGATGAACGATGAGGCGAGCCACCTACGCTGCCATCGTGACCATGACACTTGGGCTGCGCTTCTGAGGAGACACATT
146 R L E F A N G G W V M N D E A A T H Y G A I V D Q M T L G L R F L E D T F
546 TGGCAATGATGGCGACCCCGTGTGGCTGGCAGATTGACCCCTTCGGCCACTCTCGGAGCAGGCTCGCTGTTTGGCAGATGGGCTTCGACGGCTTCTCTTTGGG
182 G N D G R P R V A W H I D P F G H S R E Q A S L F A Q M G F D G F F F G
655 CGCTTGATTATCAAGATAAGTGGTACGAGTGGAGATGGAGCAGGTGTGGCGGCCAGCAGCAGCTGAAGCCCCCGGCGGACCTTCTCTGCTG
219 R L D Y Q D K W V R M Q K L E M E Q V W R A S T S L K P P T A D L T G
764 TGCTTCCCAATGGTTACAAACCGCCAAAGGAATCTGTGCTGGGATGTGCTGTGTCGATCAGCCGCTGGTGGAGGACCTTCGACGCCCGAGTACAACGCCAAGGAGCT
255 V L P N G Y N P P R N L C W D V L C V D Q P L V E D P R S P E Y N A K E L
873 GGTGATTAATCTTAAATGTGGCCACTGCCAGGGCGCGTATTACCGCACCACACACTGTGATGACCATGGGCTCGGAGTTCCTAATAGAAATGCCAATGTGG
291 V D Y F L N V A T A Q G R Y Y R T N H T V M T M G S D F Q Y E N A N M W
982 TTCAAGAACCTTGACAGCTCATCCGCTGGTAAATGCCAGCAGGCAAAAGGAAGCAGTGTCCATGTTCTCTACTCCACCCCGCTTGTACCTCTGGGAGCTGAACA
328 F K N L D K L I R L V N A Q Q A K G S S V H V L Y S T P A C Y L W E L N
1091 AGGCCAACTCACTGGTCAAGAACATGACGACTTCTTCCCTTACCGGATGGCCCCCAGCTTCTGGACCGGTACTTTTCCAGTCCGCCCGCCCTCAAACGCTA
364 K A N L T W S V K H D D F F P Y A D G P H Q F W T G Y F S S R P A L K R Y
1200 CGAGCGCTCAGCTACAACTTCTCGAGGTGTGCAACAGCTGGAGGCGGTGGTGGGCGCAACGTGGGACCTATGGCTCCGGAGACAGTGCACCCCTCAAT
400 E R L S Y N F L Q V C N Q L E A L V G L A A N V G P Y G S G D S A P L N
1309 GAGGCGATGGCTGTGCTCCAGCATCAGACGCGCTCAGCGGCACCTCCCGCCAGCAGTGGCCAAAGCAGTACGCGCCCGAGCTTGGCGCAGGCTGGGGGCTTGGCAGG
437 E A M A V L Q H H D A V S G T S R Q H V A N D Y A R Q L A A G W G P C E
1418 TTCTTCTGAGCAACGCGCTGGCGCGCTCAGAGGCTTCAAGATCACTTCACTTTTGGCAACAGCTAAACATCAGCATCTGCCGCTCAGCCAGACGCGCGCGCT
473 V L L S N A L A R L R G F K D H F T F C Q Q L N I S I C Q L N A A R F
1527 CCAGGTGATCGTTTATAATCCCTCGGGCGGAAGGTGAATTGGATGGTACGCGTCCCGCTCAGCGAAGGCGTTTCTGTTGTAAGGACCCCAATGGCAGGACAGTGGCC
509 Q V I V Y N P L R K V N W M V R L P V S E G V F V V K D P N G R T V P
1636 AGCGATGTGGTAATATTTCCAGCTCAGACAGCCAGCGCACCTCCCGAGCTGCTGTTCTCAGCTCACTGCCCGCCCTGGGCTTCCAGCCTATTTCAGTACCCAGG
546 S D V V I F P S S D S Q A H P P E L L F S A S L P A L G F S T Y S V A Q
1745 TGCTCGTGGGAAGCCCCAGGCGCGCACACAGCCATCCCAAGAAGTCTGGTCCCTGCTTTAACCATCGAAATGAGCACATCCGGGCAACGTTTGTATCTGA
582 V P R W K P Q A R A P Q P I P R R S W S P A L T I E N E H I R A T F D P D
1854 CACAGGGCTGTGATGGAGATTATGAACATGAATCAGCAACTCTGCTGCTGTTCCGCGAGACCTTCTTGTGTACAACCGCAGTATAGGTGACAAAGTGAACAG
618 T G L L M E I M N M N Q Q L L L P V R Q T F F W Y N A S I G D N E S D Q
1963 GCCTCAGGTGCTACATCTTCAGACCAACCAAGAACCGCTGCTGTGAGCGCTGGGCTCAGATCCACCTGGTGAAGACACCTTGGTGCAGGAGGTGCACAGA
655 A S G A Y I F R P N Q Q K P L P V S R W A Q I H L V K T P L V Q E V H Q
2072 ACTTCTCAGCTTGGTGTTCAGAGTGGTTCGCTGTACCCAGGACAGCGGCACCTGGAGTAGAGTGGTGGTGGGCGGATACCTGTGGGCGACCTGGGGGAAGCA
691 N F S A W C S Q V V R L Y P G Q R H L E L E W S V G P I P V G D T W G K E
2181 GGTATCAGCGCTTTTACACACCGCTGGAGACAAAGGACGCTTACACACAGCAGCAATGGCGGGAGATCCTGGAGAGGAGGCGGGATTATCGACCCACCTGAAA
727 V I S R F D T P L E T K G R F Y T D S N G R E I L E R R R D Y R P T W K
2290 CTGAACAGACGAGGCGCTGGCGAGGAACTACTATCCAGTCAACACCCGATTTACATCAGCGATGGAACATGACAGCTGACTGTGCTGACTGACCGCTCCAGGGG
764 L N Q T E P V A G N Y Y P V N T R I Y I T D G N M Q L T V L T D R S Q G
2399 GCAGCAGCTGAGAGATGGCTCGCTGGAGCTCATGGTGCACGGAAGGCTGCTGAAGGACGATGGACGCGGAGTATCGGAGCCACTAATGGAGAACGGTGGGGGGCTG
800 G S S L R D G S L E L M V H R R L L K D D G R G V S E P L M E N G S G A W
2508 GGTGCGAGGCGCCACCTGGTGTGCTGGACACAGCCAGGCTGCAGCGCGCGGACACCGGCTCTGGCGGAGCAGGAGGTCTGGCCCTCAGGTGGTGTGCTGGCCCG
836 V R G R H L V L L D T A Q A A A G H R L L A E Q E V L A P Q V V L A P
2617 GGTGGCGGCGCCCTACAATCTCGGGGCTCTCCGCGCAGCAGTCTCAGGCTCGCGAGGACCTGCCGCTCGGTGCACCTGCTCAGCTGGCCAGCTGGGGCC
873 G G G A A Y N L G A P P R T Q F S G L R R D L P P S V H L L T L A S W G
2726 CCGAAATGGTGTGCTGCGCTTGGAGCAGGTTTCCGCTAGGAGAGGATTCGCGAGTAACTGAGCGCCCGTTACCTTGAATCTGAGGGACCTGTTCTCCACCTT
909 P E M V L L R L E H Q F A V G E D S G R N L S A P V T L N L R D L F S T F
2835 CACCATACCCCGCTGCAGGAGACACGCTGGTGGCCAAACAGCTCCGCGAGGAGCCTCCAGGCTCAAGTGGACAAACACAGGCCCCACACCCCACTCCG
945 T I T R L Q E T T L V A N Q L R E A A S R L K W T T N T G P T P H Q T P
2944 TACCAGCTGGACCGGCAACATCAGCTTGAACCCATGGAATCCGCACTTCTGGGCTCAGTTCAATGGAAGGAGGTGGATGGTTAG
982 Y Q L D P A N I T L E P M E I R T F L A S V Q W K E V D G
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Human cytoplasmic mannosidase II (NM_006715)

1 ATGCGCGCAGCGCGCTTCTTGAAGCACTGGCGCACCACTTTTGAAGCGGGTGGAGAAGTTCTGTGTCGCCGATCTACTTCAACGACTGTAACTCCGCGGAGCGCTTTTGT
2 1) M A A A P F L K H W R T T T F F E R V E K F V S P I Y F T D C N L R G R I F
110 GGGCCAGCTGCCCTGTGGCTGTGCTCTCCAGGTTCTCTGACGCGGGAGGAGTCTCTCTACGAGGAGGAGCTGACGCGGGACTTCCGCCCCGCGCAGCTCGGCGCAGAGCTT
37) G A C S C P V A V L T S S F L T P E R L P Y Q E A V Q R D F R P A Q V G D S F
219 CGGACCACTAGGTGGACACTGCTGTTTCGGGTGGAGCTGACCATCCAGAGGAGTGGGTGGCGCAGGAAGTTCACTTCTGCTGGAAAGTGATGGAGAAGGCTCGGTG
73) G P T W W T C W F R V E L T I P E A W V Q E V H L C W E S D G E G L V
328 TGCGCTGATGGAGAAGCTGTCCAGGGTTTAAACAAAGAGGGTGAGAAGCAGTATGTCTGACTGCAGGCTGGGGGAAAGAGACCCCCGAAGCTCTACTCTCTATG
110) W R D G E P V Q G L T K E G E K T S Y V L T D R L G E R D P R S L T L Y
437 TGGAGTAGGCTGCATAGGGCTCTGGGGCGGGAGGGAAGCATGATTGACAGCCCTGACCGCTGAGAAGATATTCCAGCTGAGCGCGGCTGAGCTAGCTGTGCTTCCA
146) V E V A C A N G L L G A G K G S M I A A P D E K I F Q L S R A E L A V F H
546 CCGGAGTGCTCCACATGCTCTCGTGGATCTGGAGCTGCTGCTGGGATCGCAACGAGGCTCTGGGAAGGACACACGAGCGAGCTTCCAGGCGCTGTACACAGCAATCA
182) R D V H M L L V D L E L L L G I A K L G K D N Q R S F Q A L Y T A N Q
655 ATGGTGCAAGCTGTGTGACAGCTCCCGACCGCCAGAGACTCTCCAGTGCGCCAGGCGCTGGCGCTCAGGTTCTTTGGCCAAATGGGGGTGAAAGCGCAACACCACTCATG
229) M V N V C D P A Q P E T P F V A O A L A S R F T T F G Q H G G E S O H T I H
764 CCACAGGCGACTGCCACATTGATACAGCTGGCTTTGGCCCTTCAAAGAGACTGTGAGGAAATGTGCCCGGAGCTGGGTGACCGCCTGCAGCTCATGGAGCGGAACCC
255) A T G H C H I D T A W L W P F K E T C T V R K C A R S W T A L Q L M E R N P
873 TGAGTTTCATCTTCTCGCTCCGAGGCGAGCAGCTGGAATGGGTGAAGAGCTGACCTACCTGCGCTGACTCCGCACTCCAGGAGTTTGCCTGCTGGGACGTTTGTG
291) E F I F A C S Q A Q Q L E W V K S R Y P G L Y S R I G Q I D E F A C R G O F V
982 CCTGTGGGGGCACTGGGTGAAATGGATGGGAAGCTGCCAGTGGAGAGGCATGGTGAGGACGTTTTCGAGGCGCAAGACTCTTCTCTGAGGAGTTTGGGAAG
328) P V G G T G W V E M D G N L P S G E A M V R O F L Q G O N F F L Q O E F G K
1091 TGTGCTCTGAGTTCTGGCTGCCGACACCTTTGGCTACTCAGCAGAGCTCCCCAGATCATGCAGCGCTGTGGCATCAGGCGCTTCTCACCAGAAATAGAGCTGGAA
364) M C S E F W L P D T F G Y S A Q L P Q I M H G C G I R R F L T Q K L S W N
1200 TTTGGTGAACTCTTCCCAACCATACATTTTTGGGAGGGCTGGATGCTCCGCTGCTACTGTCCTCCACTCCGACCTCTCTATGGGATCGAGGCGAGCGGTG
400) L V N S F P H T T F F W E G L D G S R V L V H F P P G D S Y G M Q Q S V
1309 GAGGAGGCTCTGAAGACCTGGGCCAACACGGGACAGGGGCGGGCCACCAACAGTGCCTTCTCTTTGGCTTGGGATGGGGGTGGGCTGGCCCTCAGACACTGC
437) E E V L K T V A N N R D K G R A N H S A F L G F G D G G G G T Q T M
1418 TGGACCGCCTGAAGCGCCTGAGCAATACGGATGGGCTGCCAGGGTGAGCTATCTTCTTCAAAGACAGCTCTTCTCAGCACTGGAGAGTGACTCAGAGCAGCTGTGCAC
473) L D R L K R L S N T D G L P R A V Q L S S P R O L F S A L E S D S E O L C T
1527 GTGGGTTGGGAGCTCTCTTGAGAGCTGCACATAGGCATACACACCCATCGCCAGATCAAGAAGGGGAACCGGGAATGTAGCGGATCTGCAGCAGCTGGAGCTG
509) W V G E L F A L H N G T Y T T H A Q I K K G N R E C E R I L H D V E L
636) CTCAGTACTGGCCCTGGCCCGAGTGGCCACTTCTATACCCAGAGCCGAGCTGCAGCACTCTGGAGGCTCTCTTCTGAACAGTTCATGATGTGGTGACTG
546) L S S L A L A R S A Q F L Y P A A Q L Q H L W R L L L L N Q F H D V V T
1745 GAAGCTGCATCCAGATGGTGGCAGAGGAAGCCATGTGCCATATGAAGACATCCGTTCCCATGGCAATACACTGCTCAGCGCTGCAGCCCGACGCCCTGTGTCTGGGA
582) G S C I Q M V A E E A M C H Y E D I R S H G N T L S A A A A L C A G E
1854 GCGAGGCTCCTGAGGCGCTCTCATCTGCAACACACTGCCCTGGAAKCGGATCGAAGTGATGGCCCTGCCCAAACCGGGCGGGGCGCCACAGCTAGCCCTGTGTGACAGTG
618) P G P E G L L I V N T L P W A K R I E V M A L P K P G G A H S L A L V T V
1963 CCGACAGTAGGCTATGCTCTGTTCTCTCCCAACCTCAGCTGCAGCCCTCTGCTGCCAGAGCTGTGTCTGATGCAAGAGACTGATGGCTCCGTGACTGTGACA
655) P S M G Y A P V P P T S L Q P L P Q Q P V F V Q E T D G S V L D
2072 ATGGCATCATCCGAGTGAAGCTGGACCCAACTGGTGCCTGACCTGCTTGGTCTGGTGGCTCTGGCAGGAGGCCATTGCTGAGGCGCGCGTGGGGAACCACTTTGT
691) N G I I R V K L D P T G R L L T S L V L A S G R E A I E A G V N Q F V
2181 GCTATTGATGATGCTGCCCTGTGATGGGATGCATGGAGCTCATGAGTACCACTGGAGACAGGAAGCTGTGCTGGGCCAGGACAGGACCTGGAGCTGGGACG
727) L F D D V C L Y W D A W D V M D Y H L E T R K P V L G G A T G G A T V G G T
2290 GAGGCGCGCTCGGGGACAGCTGTTCTTGTGTACAGTACAGCCCAAGTGCAGGCTTAGCCAGAGGTTGTGCTGGACGTTGGCTGCCCTATGCTTCGCTTCCACA
764) E G G L R G S A W F L L Q I S P N S R L S Q E V V L D V G C P Y V R F H
2399 CCGAGGTACACTGGCATGAGGCCCAAGACTCTGAAGGTGGAGTTCCTGCTCGGCTGGGAGTTCCCGAGCCACCTATGAGATCCAGTTTGGGCACCTGTGACGAC
800) T E V H W H E A H K F L K V E F P A R V R S S Q A T Y E I Q F G H L R P
2508 TACCACCAACAATACCTCTTGGGACTGGGCTGATTTGAGGTGTGGGCCCATCGGCTGATGGATCTGCAGAACACGGCTTTGGGCTGGCCCTGCTCAACGACTGCAGG
836) T H Y N T S W D W A R F E V W A H R W M D L S E H G F G L A L L N D C K
2617 ATGGCGCGCTCAGTGGGAGGAGCAGTACTCTCAGCTCTCGCTCTCGGGCGGCTTAAAGCCCGGACGCTACTGCTGACACGGGCGCCAGCTAGCTTCACTATGCACCTGA
873) Y G A S V R G S I L S L S L L R A P K A P D A T D T G R H E F T Y A L
2726 TGCCGCACAAGGGCTCTTCCAGGATGCTGGCGTTATCCAAGCTGCCTACAGCTAAACTTCCCCCTGTTGGCTCTGCCAGCCCCAGCCAGCGGCCGCCACCTCTG
909) M P H K G S C T T C F D A G V I Q A A Y S L N F L L A P L A T S P A T S W
2835 GAGTGGCTTTTCCGTGTCTTACCACCGGTGATATTGAGAGAGCTCAAGCAGGCGGAGAGAGCCGCCAGCCCGCGCTCGCTGGTCTGAGGCTGATGAGGCGCCAGCG
945) S A F S V S S P A V V L E T V K Q A E S S P Q R R S L V L L R L Y E A H G
2944 AGCCACTGGAGCTGCTGGCTGACTTGTGCTGCTGGGTTTCAAGAGGCACTCTCTGCGATCTTGGAGCGACACAGACCTGCTGGCCACTTGACTTCGGGACCAACCGC
982) S H V D C W L H L S L P V Q E A I L C D L L E R P D P A G H L T S G Q P
3053 CTGAAGCTCACCTTTTCTCCCTTCAAAGTGCTGCTCGTGTGCTGCTCAGCTCCGCGCACTGAGTCCCTGGGCTGGGTTTGTGTGAGAAGGCTCTGGG
1018) P E A H L F S L P S A V P V A R A S A S A T L S P W G G F V C R L R W G
3162 ACTCTCAATTTCTGCTTCCCGACCTAA
1054) L L I S A S P A

